binding pattern of the **peptide** fragments to a reference set. A solution set refers to a set of binding reagents, or epitopes associated with such binding reagents, that can identify members of a given protein mixture or protein catalog using a minimal number of binding reagents (or epitopes corresponding to the binding reagents) based on certain constraints. The solution set can be determined using a randomized greedy algorithm. The solution set
can be refined using a local search algorithm.

ST protein **proteolysis** algorithm library computer mol assocn

IT Immunoglobulins
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(fragments F(ab); methods and systems for identifying proteins)

IT Algorithm
Computer application
Epitopes
Fluorescent substances
Labels
Microarray technology
Molecular association
Peptide library
Protein degradation
Sample preparation
Thermal decomposition
(methods and systems for identifying proteins)

IT Proteins
RL: ANT (Analyte); PRP (Properties); ANST (Analytical study)
(methods and systems for identifying proteins)

IT **Antibodies**
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(methods and systems for identifying proteins)

IT **Antibodies**
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(single chain, ScFv; methods and systems for identifying proteins)

IT 9031-96-3, Peptidase
RL: NUU (Other use, unclassified); USES (Uses)
(I, Staphylococcal; methods and systems for identifying proteins)

IT 64-18-6, Formic acid, uses **506-68-3, Cyanogen bromide** ((CN)Br) 7803-49-8, Hydroxylamine, uses **9001-75-6, Pepsin 9002-04-4, Thrombin** 9002-05-5, Factor Xa **9002-07-7, Trypsin** **9004-07-3, Chymotrypsin** 9028-00-6, Clostridiopeptidase B 27323-35-9, Iodosobenzoic acid 27933-36-4, BNPS-skatole **30211-77-9** 39450-01-6 55576-49-3, Endoproteinase Asp-N 72162-84-6, Proline-endopeptidase 122191-40-6, Caspase 1 123175-81-5, Endoproteinase Arg-C 123175-82-6, Endoproteinase Lys-C 137010-42-5, Glutamyl endopeptidase 143180-74-9, Granzyme B 169592-56-7, Caspase 3 179241-78-2, Caspase 8 180189-96-2, Caspase 9 182372-14-1, Caspase 2 182372-15-2, Caspase 6 182762-08-9, Caspase 4 189088-85-5, Caspase 10 189258-14-8, Caspase 7 192465-11-5, Caspase 5
RL: NUU (Other use, unclassified); USES (Uses)
(methods and systems for identifying proteins)

L51 ANSWER 2 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN
AN **2002:615643** HCAPLUS
DN **137:165775**
TI **Peptide** or protein microassay method and apparatus
IN Diamond, Scott L.
PA University of Pennsylvania, USA
SO PCT Int. Appl., 52 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C07K

CC **9-1** (**Biochemical Methods**)
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2002062821	A2	20020815	WO 2002-US2262	20020124
	WO 2002062821	A3	20030220		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

	US 2002142351	A1	20021003	US 2001-36066	20011107
PRAI	US 2001-266042P	P	20010202		
	US 2001-309999P	P	20010803		
	US 2001-313368P	P	20010817		
	US 2001-313377P	P	20010817		
	US 2001-313380P	P	20010817		
	US 2001-322619P	P	20010917		
	US 2001-36066	A	20011107		

AB A **peptide** or protein microassay method and apparatus in which a wide variety of chromogenic or fluorogenic **peptide** or protein substrates of interest are individually suspended or dissolved in a hydrophilic carrier, with aliquots of each substrate being deposited in an **array** or **microarray** of reaction loci, or "dots.". Each dot, therefore, provides an individual reaction vessel containing the **peptide** or protein of interest, to which a biol. sample may be applied for assay purposes. The sample is applied to the **array** or **microarray** of dots by one of a variety of focused sample application techniques, including aerosolizing or misting of the sample, or target application of the sample, onto each dot without creating fluid channels between the dots which would cause cross-contamination.

ST **peptide** protein microassay app

IT **Enzymes**, uses
RL: ARG (Analytical reagent use); DEV (Device component use); TEM (Technical or engineered material use); ANST (Analytical study); USES (Uses)
(activators; **peptide** or protein microassay method and apparatus)

IT Biological materials
(anal. of; **peptide** or protein microassay method and apparatus)

IT Materials processing
(applicators, computer-controlled dot; **peptide** or protein microassay method and apparatus)

IT Glycols, analysis
Hexoses
Polysaccharides, analysis
RL: ARU (Analytical role, unclassified); DEV (Device component use); TEM (Technical or engineered material use); ANST (Analytical study); USES (Uses)
(as carrier for **peptide** or protein; **peptide** or protein microassay method and apparatus)

IT Aerosols
(computer-controlled device for generation of; **peptide** or protein microassay method and apparatus)

IT Control apparatus
(computerized; **peptide** or protein microassay method and apparatus)

IT Fans
(exhaust/filtration; **peptide** or protein microassay method and apparatus)

IT Fluorescent substances
(fluorogen; **peptide** or protein microassay method and apparatus)
IT Carriers
(hydrophilic; **peptide** or protein microassay method and apparatus)
IT Electrostatic charge
(in capture of mist on **microarray**; **peptide** or protein microassay method and apparatus)
IT **Enzymes**, uses
RL: ARG (Analytical reagent use); DEV (Device component use); TEM (Technical or engineered material use); ANST (Analytical study); USES (Uses)
(inhibitors; **peptide** or protein microassay method and apparatus)
IT Cell
(lysates; **peptide** or protein microassay method and apparatus)
IT Syringes
(microsyringes; **peptide** or protein microassay method and apparatus)
IT Pumps
(multiple pos. displacement microsyringe; **peptide** or protein microassay method and apparatus)
IT Glass, uses
RL: DEV (Device component use); TEM (Technical or engineered material use); USES (Uses)
(nonporous chip or slide containing; **peptide** or protein microassay method and apparatus)
IT Biochemical molecules
Blood analysis
Blood plasma
Buffers
Color formers
Computer program
Flowmeters
Ink-jet printer heads
Liposomes
Microarray technology
Protein microarray technology
Ultrasonic transducers
(**peptide** or protein microassay method and apparatus)
IT Blood-coagulation factors
RL: ANT (Analyte); ANST (Analytical study)
(**peptide** or protein microassay method and apparatus)
IT **Antibodies**
Coenzymes
Lipids, uses
Nucleic acids
Peptides, uses
Proteins
RL: ARG (Analytical reagent use); DEV (Device component use); TEM (Technical or engineered material use); ANST (Analytical study); USES (Uses)
(**peptide** or protein microassay method and apparatus)
IT Polymers, uses
RL: DEV (Device component use); TEM (Technical or engineered material use); USES (Uses)
(polyalkylene, nonporous chip or slide containing; **peptide** or protein microassay method and apparatus)
IT Alcohols, analysis
RL: ARU (Analytical role, unclassified); DEV (Device component use); TEM (Technical or engineered material use); ANST (Analytical study); USES (Uses)
(polyhydric, alkylene polyols, as carrier for **peptide** or protein; **peptide** or protein microassay method and apparatus)
IT Polyoxyalkylenes, analysis

RL: ARU (Analytical role, unclassified); DEV (Device component use); TEM (Technical or engineered material use); ANST (Analytical study); USES (Uses)
(polymers, as carrier for **peptide** or protein; **peptide** or protein microassay method and apparatus)

IT **Enzymes**, analysis
RL: ANT (Analyte); ARG (Analytical reagent use); DEV (Device component use); TEM (Technical or engineered material use); ANST (Analytical study); USES (Uses)
(reaction components; **peptide** or protein microassay method and apparatus)

IT Carbohydrates, analysis
RL: ARU (Analytical role, unclassified); DEV (Device component use); TEM (Technical or engineered material use); ANST (Analytical study); USES (Uses)
(saccharides, as carrier for **peptide** or protein; **peptide** or protein microassay method and apparatus)

IT Nozzles
(spray; **peptide** or protein microassay method and apparatus)

IT Nozzles
Spray atomizers
(ultrasonic; **peptide** or protein microassay method and apparatus)

IT 50-69-1D, Ribose, carbohydrates 56-81-5, Glycerol, analysis 107-21-1, 1,2-Ethanediol, analysis 513-85-9, 2,3-Butanediol 9004-54-0, Dextran, analysis 25322-68-3D, Polyethylene glycol, polymers 53106-52-8D, Pentose, carbohydrates 106392-12-5
RL: ARU (Analytical role, unclassified); DEV (Device component use); TEM (Technical or engineered material use); ANST (Analytical study); USES (Uses)
(as carrier for **peptide** or protein; **peptide** or protein microassay method and apparatus)

IT 186322-81-6, Caspase
RL: ANT (Analyte); ANST (Analytical study)
(**microarray** substrate for; **peptide** or protein microassay method and apparatus)

IT 7440-21-3, Silicon, uses 7631-86-9, Silica, uses 9003-53-6, Polystyrene 14808-60-7, Quartz, uses
RL: DEV (Device component use); TEM (Technical or engineered material use); USES (Uses)
(nonporous chip or slide containing; **peptide** or protein microassay method and apparatus)

IT 9001-90-5, Plasmin **9002-04-4, Thrombin** 9002-05-5, Blood coagulation factor Xa 139639-23-9, Tissue plasminogen activator 410538-33-9, Plasma kallikrein
RL: ANT (Analyte); ANST (Analytical study)
(**peptide** or protein microassay method and apparatus)

IT 65147-04-8 73554-84-4
RL: ARG (Analytical reagent use); DEV (Device component use); PRP (Properties); TEM (Technical or engineered material use); ANST (Analytical study); USES (Uses)
(**peptide** or protein microassay method and apparatus)

L51 ANSWER 3 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN
AN 2002:538187 HCAPLUS
DN 137:106076
TI **Peptides** representative of **polypeptides** of interest and **antibodies** directed there against, and methods, systems and kits for generating and utilizing each
IN **Katz, Emil Israel**
PA Israel
SO Eur. Pat. Appl., 124 pp.
CODEN: EPXXDW
DT **Patent**

LA English
IC ICM **G06F019-00**
ICS **G01N033-53**; **G01N033-68**; C12P021-06; C07K016-18; C07K001-12; C07K002-00
CC **9-16** (**Biochemical Methods**)
Section cross-reference(s): 6, 14, 15
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	EP 1223534	A1	20020717	EP 2002-75095	20020111
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
	US 2002137119	A1	20020926	US 2001-982172	20011019
	JP 2002360278	A2	20021217	JP 2002-4906	20020111
PRAI	IL 2001-140881	A	20010114		
	US 2001-982172	A	20011019		

AB A method of generating a set of amino acid sequences representative of at least one **polypeptide** of interest is provided. Also provided are kits and methods of using such **peptides** and **antibodies** generated there against for detecting the presence, absence or severity of a disease. The protein sequences of P-glycoprotein and of mitoxantrone resistance protein (MXR) were **computationally analyzed** to obtain tryptic amino acid sequences for each protein. These sequences were scanned for homol. to all known protein sequences. Only a portion of the tryptic **peptide** sequences were found to be unique. These unique tryptic sequences were further **analyzed** for immunogenicity. Selected **peptides** were synthesized and used to generate **antibodies**.

ST **peptide** representative protein **antibody** system kit; amino acid sequence representative protein; disease diagnosis **peptide antibody**; P glycoprotein unique immunogenic tryptic **peptide antibody**; mitoxantrone resistance protein unique immunogenic tryptic **peptide**

IT Amino acids, properties
RL: PRP (Properties)
(compns.; **peptides** representative of **polypeptides** of interest and **antibodies** and methods and systems and test kits)

IT Protein sequences
(homol.; **peptides** representative of **polypeptides** of interest and **antibodies** and methods and systems and test kits)

IT **Antibodies**
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(immobilized; **peptides** representative of **polypeptides** of interest and **antibodies** and methods and systems and test kits)

IT **Antibodies**
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(labeled; **peptides** representative of **polypeptides** of interest and **antibodies** and methods and systems and test kits)

IT **Peptides, biological studies**
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(labeled; **peptides** representative of **polypeptides** of interest and **antibodies** and methods and systems and test kits)

IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(mitoxantrone resistant; **peptides** representative of

polypeptides of interest and **antibodies** and methods and systems and test kits)

IT **Antibodies**
RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(monoclonal; **peptides** representative of **polypeptides** of interest and **antibodies** and methods and systems and test kits)

IT **Computers**
Databases
Disease, animal
Electric charge
Heterogeneity
Human
Hydrophilicity
Hydrophobicity
Information systems
Length
Microarray technology
Molecular weight
Polarity
Post-translational processing
Protein microarray technology
Protein sequences
Solubility
Test kits
(**peptides** representative of **polypeptides** of interest and **antibodies** and methods and systems and test kits)

IT P-glycoproteins
RL: ANT (Analyte); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); PREP (Preparation)
(**peptides** representative of **polypeptides** of interest and **antibodies** and methods and systems and test kits)

IT Proteins
RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); RCT (Reactant); ANST (Analytical study); BIOL (Biological study); RACT (Reactant or reagent)
(**peptides** representative of **polypeptides** of interest and **antibodies** and methods and systems and test kits)

IT **Antibodies**
RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(**peptides** representative of **polypeptides** of interest and **antibodies** and methods and systems and test kits)

IT **Peptides, biological studies**
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); SPN (Synthetic preparation); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(**peptides** representative of **polypeptides** of interest and **antibodies** and methods and systems and test kits)

IT Antigens
RL: PRP (Properties)
(**peptides** representative of **polypeptides** of interest and **antibodies** and methods and systems and test

kits)
IT Secondary structure
(protein; **peptides** representative of **polypeptides** of interest and **antibodies** and methods and systems and test kits)
IT **Information systems**
(storage; **peptides** representative of **polypeptides** of interest and **antibodies** and methods and systems and test kits)
IT 442515-48-2
RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study)
(P-glycoprotein **peptide**, amino acid sequence; **peptides** representative of **polypeptides** of interest and **antibodies** and methods and systems and test kits)
IT 442515-26-6 442515-29-9 442598-58-5
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence, P-glycoprotein computer-generated tryptic **peptide** not found in other human proteins; **peptides** representative of **polypeptides** of interest and **antibodies** and methods and systems and test kits)
IT 442515-49-3P 442515-51-7P
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); SPN (Synthetic preparation); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence, immunogenic P-glycoprotein **peptide**; **peptides** representative of **polypeptides** of interest and **antibodies** and methods and systems and test kits)
IT 442515-50-6P
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); SPN (Synthetic preparation); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence, immunogenic **peptide** of mitoxantrone resistant protein; **peptides** representative of **polypeptides** of interest and **antibodies** and methods and systems and test kits)
IT 442515-34-6 442515-35-7 442598-62-1
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence, mitoxantrone resistant protein computer-generated tryptic **peptide** not found in other human proteins; **peptides** representative of **polypeptides** of interest and **antibodies** and methods and systems and test kits)
IT **506-68-3, Cyanogen bromide 9001-75-6**
, Pepsin 9001-92-7, Proteinase **9002-04-4,**
Thrombin 9002-07-7, Trypsin 9004-06-2
, Elastase 9004-07-3, Chymotrypsin 9014
-01-1, Subtilisin 30211-77-9 66676-43-5
, V8 Protease
RL: CAT (Catalyst use); MSC (Miscellaneous); USES (Uses)
(computationally generating protein cleavage products from; **peptides** representative of **polypeptides** of interest and **antibodies** and methods and systems and test kits)
IT 58-85-5D, Biotin, conjugates with P-glycoprotein **peptide** target of monoclonal **antibody**
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(**peptides** representative of **polypeptides** of interest and **antibodies** and methods and systems and test kits)
IT 155024-01-4 231960-03-5 442515-15-3 442515-16-4 442515-17-5
442515-18-6 442515-19-7 442515-20-0 442515-21-1 442515-22-2
442515-23-3 442515-24-4 442515-25-5 442515-27-7 442515-28-8

442515-30-2 442515-31-3 442515-32-4 442515-33-5 442515-36-8
442515-37-9 442515-38-0 442515-39-1 442515-40-4 442515-41-5
442515-42-6 442515-43-7 442515-44-8 442515-45-9 442515-46-0
442515-47-1 442598-56-3 442598-57-4 442598-59-6 442598-60-9
442598-61-0 442598-63-2 443301-11-9 443301-12-0 443301-13-1
443301-14-2 443301-15-3 443301-16-4 443301-17-5 443301-18-6
443301-19-7 443301-20-0 443301-21-1 443301-22-2 443301-23-3
443301-24-4 443301-25-5 443301-26-6 443301-27-7 443301-28-8
443301-29-9 443301-30-2 443301-31-3 443301-32-4 443301-33-5
443301-34-6 443301-35-7 443301-36-8 443301-37-9 443301-38-0
443301-39-1 443301-40-4 443301-41-5 443301-42-6 443301-43-7
443301-44-8 443301-45-9 443301-46-0 443301-47-1 443301-48-2
443301-49-3 443301-50-6 443301-51-7 443301-52-8 443301-53-9
443301-54-0 443301-55-1 443301-56-2 443301-57-3 443301-58-4
443301-59-5 443301-60-8 443301-61-9 443301-62-0 443301-63-1
443301-64-2 443301-65-3 443301-66-4 443301-67-5 443301-68-6
443301-69-7 443301-70-0 443301-71-1 443301-72-2 443301-73-3
443301-74-4 443301-75-5 443301-76-6 443301-77-7 443301-78-8
443301-79-9 443301-80-2 443301-81-3 443301-82-4 443301-83-5
443301-84-6 443301-85-7 443301-86-8 443301-87-9 443301-88-0
443301-89-1 443301-90-4 443301-91-5 443301-92-6 443301-93-7
443301-94-8 443301-95-9 443301-96-0 443301-97-1 443301-98-2
443301-99-3 443302-00-9 443302-01-0 443302-02-1 443302-03-2
443302-04-3 443302-05-4 443302-06-5 443302-07-6 443378-12-9
443378-13-0
RL: PRP (Properties)
(unclaimed sequence; **peptides** representative of **polypeptides** of interest and **antibodies** directed there against, and methods, systems and kits for generating and utilizing each)

IT 443301-10-8
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(unclaimed; **peptides** representative of **polypeptides** of interest and **antibodies** directed there against, and methods, systems and kits for generating and utilizing each)

RE.CNT 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD

RE

(1) Cianfriglia, M; WO 9325700 A 1993 HCAPLUS
(2) Jameson, B; COMPUTER APPLICATIONS IN THE BIOSCIENCES 1988, V4(1), P181 HCAPLUS
(3) Maksyutov, A; COMPUTER APPLICATIONS IN THE BIOSCIENCES 1993, V9(3), P291 HCAPLUS
(4) Mark, C; METHODS IN MOLECULAR BIOLOGY 1994, V36, P193
(5) Univ California; WO 9502188 A 1995 HCAPLUS
(6) Univ California; WO 0024777 A 2000 HCAPLUS
(7) van der Straeten, K; http://delphi.phys.univ-tours.fr/Prolysis/cutter.html 1998-1999
(8) Winthrop University Hospital; WO 9964621 A 1999 HCAPLUS
(9) Wolf, H; COMPUTER APPLICATIONS IN THE BIOSCIENCES 1988, V4(1), P187 HCAPLUS

L51 ANSWER 4 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN
AN **2002:466235** HCAPLUS
DN **137:17414**
TI System for multiplexed protein expression and activity assay
IN Monforte, Joseph A.
PA HK Pharmaceuticals, Inc., USA
SO PCT Int. Appl., 67 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C12Q001-68
ICS G01N033-68; G01N033-543; G01N033-569

CC **9-1 (Biochemical Methods)**
Section cross-reference(s): 3, 6

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2002048403	A2	20020620	WO 2001-US48023	20011211
	WO 2002048403	A3	20030130		
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	AU 2002030788	A5	20020624	AU 2002-30788	20011211
	EP 1343914	A2	20030917	EP 2001-991033	20011211
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
PRAI	US 2000-254958P	P	20001211		
	WO 2001-US48023	W	20011211		

AB The invention concerns a system for analyzing expression levels and activity of a plurality of proteins. A bio-displayed **polypeptide** binding component associated with a predetd. marker is used to bind the proteins of interest. The predetd. marker components are then amplified and detected in a high throughput manner.

ST high throughput screening protein phage library genetic methods marker

IT Genetic methods
(Qβ-replicase amplification; System for multiplexed protein expression and activity assay)

IT Analytical apparatus
Animal tissue
Animal tissue culture
Bacteriophage
Bacterium (genus)
Baculoviridae
Blood analysis
Body fluid
Coliphage M13
Coliphage T4
Coliphage λ
Computer program
Computers
Databases
Electrochemistry
Electrophoresis
Genetic markers
Genome
High throughput screening
Mass spectrometers
Mass spectrometry
Membrane filters
Microarray technology
Microspheres
Microtiter plates
Multivariate analysis
NMR spectroscopy
Nucleic acid hybridization
Optical detectors
Organ, animal
PCR (polymerase chain reaction)

Phage display library
Pipes and Tubes
Plates
Spheres
Time-of-flight mass spectrometry
(System for multiplexed protein expression and activity assay)

IT **Enzymes**, analysis
RL: ANT (Analyte); ARG (Analytical reagent use); PRP (Properties); ANST (Analytical study); USES (Uses)
(System for multiplexed protein expression and activity assay)

IT Proteins
RL: ANT (Analyte); PRP (Properties); ANST (Analytical study)
(System for multiplexed protein expression and activity assay)

IT **Antibodies**
Avidins
Ligands
Nucleic acids
Receptors
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(System for multiplexed protein expression and activity assay)

IT Polyamides, uses
RL: DEV (Device component use); USES (Uses)
(System for multiplexed protein expression and activity assay)

IT Proteins
RL: ANT (Analyte); PRP (Properties); ANST (Analytical study)
(cancer-related; System for multiplexed protein expression and activity assay)

IT Luminescence, chemiluminescence
(electrochemiluminescence; System for multiplexed protein expression and activity assay)

IT Gene
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(expression; System for multiplexed protein expression and activity assay)

IT Immunoglobulins
RL: ARG (Analytical reagent use); PRP (Properties); ANST (Analytical study); USES (Uses)
(fragments; System for multiplexed protein expression and activity assay)

IT Genetic methods
(ligase chain reaction; System for multiplexed protein expression and activity assay)

IT Animal cell
(lysate; System for multiplexed protein expression and activity assay)

IT Apparatus
(**microarray**; System for multiplexed protein expression and activity assay)

IT Laser ionization mass spectrometry
(photodesorption, matrix-assisted; System for multiplexed protein expression and activity assay)

IT Laser desorption mass spectrometry
(photoionization, matrix-assisted; System for multiplexed protein expression and activity assay)

IT Surface plasmon
(resonance; System for multiplexed protein expression and activity assay)

IT Microscopes
(slides; System for multiplexed protein expression and activity assay)

IT **Enzymes**, analysis
RL: ANT (Analyte); PRP (Properties); ANST (Analytical study)
(substrate; System for multiplexed protein expression and activity assay)

IT 58-85-5, Biotin 9013-20-1, Streptavidin

RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(System for multiplexed protein expression and activity assay)
IT 9004-70-0, Nitrocellulose
RL: DEV (Device component use); USES (Uses)
(System for multiplexed protein expression and activity assay)
IT 7440-21-3, Silicon, uses
RL: DEV (Device component use); USES (Uses)
(chip; System for multiplexed protein expression and activity assay)

L51 ANSWER 5 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN
AN **2002:293977** HCAPLUS
DN **136:306442**
TI Method for determining mass altering moiety in **peptides**
IN Smilansky, Zeev
PA Compugen Ltd., Israel
SO PCT Int. Appl., 46 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM G01N033-68
ICS G06F019-00; C12Q001-37
CC **9-16** (**Biochemical Methods**)
Section cross-reference(s): 6
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2002031509	A2	20020418	WO 2001-IL944	20011011
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	AU 2002010884	A5	20020422	AU 2002-10884	20011011
PRAI	IL 2000-138946	A	20001011		
	WO 2001-IL944	W	20011011		

AB The invention concerns methods for detecting, analyzing, and interpreting differences between an assayed **peptide** and a corresponding database **peptide**. This means that once a **peptide** was identified, with a high probability (a high score), as being similar to a specific corresponding database **peptide** in accordance with any methods known in the art, it is possible by the method of the invention, to identify specific differences between the assayed **peptide** and the corresponding database **peptide**, including masses of the altering moieties or sequences, their identities, and location within the **peptide**. Further, the invention concerns a method for determining the mass of a mass altering moiety, and for identifying a cleavage altering sequence, wherein the mass altering moiety or a cleavage altering sequence is present in an assayed **peptide** and is absent from a corresponding database **peptide**, or is present in a database **peptide** and is absent from an assayed **peptide**.
ST **peptide** database fragment mass altering digestion mass spectrometry
IT Functional groups
(acidic groups; method for determining mass altering moiety in **peptides**)
IT Mass
(alteration of; method for determining mass altering moiety in **peptides**)
IT **Information systems**

(database; method for determining mass altering moiety in **peptides**)
IT Sample preparation
(in vitro; method for determining mass altering moiety in **peptides**)
IT Functional groups
(lipidic; method for determining mass altering moiety in **peptides**)
IT Acetylation
Acyl groups
Amidation
Apparatus
Chromatography
Digestion, chemical
Electrophoresis
Error
Farnesylation
Formylation
Genome
Hydroxylation
Immunoassay
Mass spectrometry
Methylation
Microarray technology
Mutation
Myristoylation
Phosphorylation
Post-translational processing
Protein sequences
RNA editing
RNA splicing
Strain
Sulfation
Test kits
Time-of-flight mass spectrometry
(method for determining mass altering moiety in **peptides**)
IT **Peptides, analysis**
RL: ANT (Analyte); PRP (Properties); ANST (Analytical study)
(method for determining mass altering moiety in **peptides**)
IT **Antibodies**
RL: ARG (Analytical reagent use); DEV (Device component use); ANST (Analytical study); USES (Uses)
(method for determining mass altering moiety in **peptides**)
IT Proteins
RL: ARG (Analytical reagent use); DEV (Device component use); ANST (Analytical study); USES (Uses)
(method for determining mass altering moiety in **peptides**)
IT Flavins
RL: ARU (Analytical role, unclassified); PRP (Properties); ANST (Analytical study)
(method for determining mass altering moiety in **peptides**)
IT Laser ionization mass spectrometry
(photodesorption, matrix-assisted; method for determining mass altering moiety in **peptides**)
IT Laser desorption mass spectrometry
(photoionization, matrix-assisted; method for determining mass altering moiety in **peptides**)
IT Amidation
(retro; method for determining mass altering moiety in **peptides**)
IT Genetic polymorphism
(single nucleotide; method for determining mass altering moiety in **peptides**)
IT Functional groups
(sugars; method for determining mass altering moiety in **peptides**)
IT Alkenylation
(tetramethylhexadecatetraenylation; method for determining mass altering

moiety in **peptides**)
IT 54-47-7, Pyridoxal phosphate 58-85-5, Biotin 7704-34-9D, Sulphur, oxidation products
RL: ARU (Analytical role, unclassified); PRP (Properties); ANST (Analytical study)
(method for determining mass altering moiety in **peptides**)
IT **506-68-3, Cyanogen bromide** 9001-92-7, Proteinase **9002-07-7, Trypsin 9004-06-2, Elastase 9004-07-3, Chymotrypsin** 9073-78-3, Thermolysin 55576-49-3, Endoproteinase AspN 123175-82-6, Endopeptidase Lys-C 137010-42-5, Endopeptidase Glu-C
RL: NUU (Other use, unclassified); USES (Uses)
(method for determining mass altering moiety in **peptides**)
IT 409415-40-3
RL: PRP (Properties)
(unclaimed sequence; method for determining mass altering moiety in **peptides**)

L51 ANSWER 6 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN
AN **2002:241096** HCAPLUS
DN **136:259600**
TI Detection of **peptides**
IN Barry, Richard; Platt, Albert Edward; Scrivener, Elaine; Soloviev, Mikhail; Terrett, Johnathan Alexander
PA Oxford Glycosciences (UK) Ltd., UK
SO PCT Int. Appl., 63 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM G01N033-68
CC **9-16** (**Biochemical Methods**)
Section cross-reference(s): 14
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2002025287	A2	20020328	WO 2001-GB4182	20010919
	WO 2002025287	A3	20030123		
	WO 2002025287	C1	20030313		
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	AU 2001090062	A5	20020402	AU 2001-90062	20010919
	US 2002055186	A1	20020509	US 2001-956751	20010919
	EP 1320754	A2	20030625	EP 2001-969937	20010919
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
PRAI	GB 2000-22978	A	20000919		
	US 2000-255364P	P	20001213		
	WO 2001-GB4182	W	20010919		

AB A method for determining the presence of one or more proteins of interest in a sample, which method comprises the step of: (c) submitting the sample to conditions that allow fragmentation of the protein into target **peptide** fragments; and (d) contacting the target **peptide** fragments with an **array** of capture agents immobilized on a solid support, the capture agents comprising those that recognize a target protein fragment; whereby the binding of the target **peptide** fragments with the capture agents is indicative of the presence of the

protein(s) in the sample. A device comprising such an **array**, and its production, are also described.

ST detection **peptide**

IT Reagents
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(Capture agents; detection of **peptides**)

IT Bond cleavage
(**Enzymic**; detection of **peptides**)

IT Cell adhesion molecules
RL: ANT (Analyte); CPS (Chemical process); PEP (Physical, engineering or chemical process); ANST (Analytical study); PROC (Process)
(VCAM; detection of **peptides**)

IT Nervous system, disease
(central; detection of **peptides**)

IT Bond
(covalent; detection of **peptides**)

IT Mental disorder
(depression; detection of **peptides**)

IT Affinity
Analytical apparatus
Animal cell
Apoptosis
Databases
Dendritic cell
Diagnosis
Disease, animal
Fragmentation reaction
Functional groups
Hydrogels
Hyperplasia
Immobilization, molecular
Labels
Mammary gland, neoplasm
Mass spectrometry
Multivariate analysis
Neoplasm
Phenotypes
Protein sequences
Samples
Solids
(detection of **peptides**)

IT Proteome
RL: ANT (Analyte); DGN (Diagnostic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(detection of **peptides**)

IT **Peptides, analysis**
Proteins
RL: ANT (Analyte); DGN (Diagnostic use); RCT (Reactant); ANST (Analytical study); BIOL (Biological study); RACT (Reactant or reagent); USES (Uses)
(detection of **peptides**)

IT **Antibodies**
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(detection of **peptides**)

IT Glass, analysis
RL: ARU (Analytical role, unclassified); DEV (Device component use); ANST (Analytical study); USES (Uses)
(detection of **peptides**)

IT Gene
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(expression; detection of **peptides**)

IT Liver, neoplasm
(hepatoma; detection of **peptides**)

IT Toxicity

(hepatotoxicity; detection of **peptides**)
IT Protein sequence analysis
(mass spectrometric; detection of **peptides**)
IT Neoplasm
(metastasis; detection of **peptides**)
IT Mass spectrometry
(protein sequence anal.; detection of **peptides**)
IT Post-translational processing
(**proteolytic**; detection of **peptides**)
IT Albumins, analysis
RL: ANT (Analyte); ANST (Analytical study)
(serum; detection of **peptides**)
IT Liver
(toxicity; detection of **peptides**)
IT 62229-50-9, Egf
RL: ANT (Analyte); PEP (Physical, engineering or chemical process); PYP (Physical process); ANST (Analytical study); PROC (Process)
(detection of **peptides**)
IT 9003-05-8, Polyacrylamide 9012-36-6, Agarose
RL: ARU (Analytical role, unclassified); ANST (Analytical study)
(detection of **peptides**)
IT 7440-21-3, Silicon, analysis
RL: ARU (Analytical role, unclassified); DEV (Device component use); ANST (Analytical study); USES (Uses)
(detection of **peptides**)
IT 9001-92-7, **Proteolytic enzyme**
RL: CAT (Catalyst use); USES (Uses)
(detection of **peptides**)

L51 ANSWER 7 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN
AN **2001:452914** HCAPLUS
DN **135:58127**
TI Cell **arrays** and the uses thereof
IN Li, Ronghao; Mather, Jennie P.
PA Biomosaic Systems, Inc., USA
SO PCT Int. Appl., 54 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM B01J019-00
ICS G01N033-543; G01N033-68; G01N033-50; G01N001-36
CC **9-1** (**Biochemical Methods**)
Section cross-reference(s): 3, 14
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2001043869	A2	20010621	WO 2000-US34010	20001215
	WO 2001043869	A3	20011129		
	W: AU, CA, JP				
	RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR				
	US 6406840	B1	20020618	US 1999-466011	19991217
	EP 1239950	A2	20020918	EP 2000-984413	20001215
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, CY, TR				
	JP 2003516747	T2	20030520	JP 2001-544993	20001215
	US 2002197656	A1	20021226	US 2002-192273	20020709
PRAI	US 1999-466011	A	19991217		
	WO 2000-US34010	W	20001215		
	US 2001-947238	A3	20010905		

AB The present invention provides cell **arrays** comprising a plurality of tubes containing populations of cells that are immobilized therein. The **arrays** are particularly useful for conducting

comparative cell-based **analyses**. Specifically, the subject **arrays** allow protein-protein interactions to be studied in multiple types of cell simultaneously. The **arrays** also support simultaneous detection of the differential expression of a target polynucleotide in a multiplicity of cell types derived from multiple subjects. The subject **arrays** further permit high throughput screening for candidate modulators of a signal transduction pathway of interest. Further provided by the invention are kits, **computer** -implemented methods and systems for conducting the comparative cell-based **analyses**.

ST cell **array**

IT Apparatus
(Cell **arrays**; cell **arrays** and uses thereof)

IT Receptors
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(Cell surface; cell **arrays** and uses thereof)

IT Apparatus
(Data storage; cell **arrays** and uses thereof)

IT Ligands
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(Receptor; cell **arrays** and uses thereof)

IT Analysis
Animal cell
Animal cell line
Animal tissue
Bacteria (Eubacteria)
Bladder
Blood
Body fluid
Bone
Brain
Cell cycle
Cell nucleus
Chemicals
Computer application
Denaturation
Development, mammalian postnatal
Disease, animal
Embryo, animal
Esophagus
Eukaryote (Eukaryotae)
Fruit fly
Genetic engineering
Genotypes
Hair
Heart
Immobilization, biochemical
Interface
Intestine
Isotope indicators
Kidney
Length
Liver
Luminescent substances
Lung
Mammary gland
Mouse
Muscle
Neoplasm
Nerve
Nucleic acid hybridization
Ovary
Pancreas

Pipes and Tubes
Prokaryote
Protein motifs
Rat
Semiconductor materials
Signal transduction, biological
Skin
Spinal cord
Spleen
Staining, biological
Stomach
Test kits
Testis
Thymus gland
Uterus
Worm
Yeast
(cell **arrays** and uses thereof)

IT Chaperonins
Peptides, analysis
RL: ANT (Analyte); ANST (Analytical study)
(cell **arrays** and uses thereof)

IT Proteins, general, analysis
RL: ANT (Analyte); ARG (Analytical reagent use); BSU (Biological study, unclassified); RCT (Reactant); ANST (Analytical study); BIOL (Biological study); RACT (Reactant or reagent); USES (Uses)
(cell **arrays** and uses thereof)

IT **Antibodies**
DNA
Enzymes, uses
Probes (nucleic acid)
RNA
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(cell **arrays** and uses thereof)

IT Immune complexes
RL: ARU (Analytical role, unclassified); FMU (Formation, unclassified); ANST (Analytical study); FORM (Formation, nonpreparative)
(cell **arrays** and uses thereof)

IT Polynucleotides
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(cell **arrays** and uses thereof)

IT Glass, uses
Metals, uses
Plastics, uses
RL: DEV (Device component use); USES (Uses)
(cell **arrays** and uses thereof)

IT Cytoplasm
(cytosol; cell **arrays** and uses thereof)

IT Embryo, animal
(ectoderm; cell **arrays** and uses thereof)

IT Embryo, animal
(entoderm; cell **arrays** and uses thereof)

IT Gene
(expression, Differential; cell **arrays** and uses thereof)

IT Immunoassay
(immunol. staining; cell **arrays** and uses thereof)

IT Drug delivery systems
(immunoliposomes; cell **arrays** and uses thereof)

IT Drug delivery systems
(immunotoxins; cell **arrays** and uses thereof)

IT Animal cell
(mammalian; cell **arrays** and uses thereof)

IT Proteins, specific or class
RL: ANT (Analyte); ANST (Analytical study)
(membrane; cell **arrays** and uses thereof)
IT Embryo, animal
(mesoderm; cell **arrays** and uses thereof)
IT **Information systems**
(storage; cell **arrays** and uses thereof)
IT Antigens
RL: ANT (Analyte); ANST (Analytical study)
(surface; cell **arrays** and uses thereof)
IT 9004-34-6, Cellulose, uses 9004-70-0, Nitrocellulose
RL: DEV (Device component use); USES (Uses)
(cell **arrays** and uses thereof)

L51 ANSWER 8 OF 8 HCAPLUS COPYRIGHT 2003 ACS on STN
AN **2000:513839** HCAPLUS
DN **133:132087**
TI Multifunctional and multispectral biosensor devices, production and methods of use
IN Vo-Dinh, Tuan
PA Lockheed Martin Energy Research Corporation, USA
SO PCT Int. Appl., 106 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C12Q001-68
CC **9-1** (**Biochemical Methods**)
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000043552	A2	20000727	WO 2000-US2051	20000125
WO 2000043552	A3	20001102		
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2358699	AA	20000727	CA 2000-2358699	20000125
EP 1151139	A2	20011107	EP 2000-905769	20000125
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
PRAI US 1999-236758	A	19990125		
WO 2000-US2051	W	20000125		

AB Disclosed are advanced multifunctional biochip devices capable of specifically detecting and quantitating multiple biomol. target compds., such as **polypeptides**, polynucleotides, and other intracellular and extracellular biomols. In illustrative embodiments, the miniaturized multifunctional biosensor device comprises multiple biol. sensing elements, excitation micro-lasers, a sampling waveguide equipped with optical fluorescence detectors, integrated electro-optics, a bio-telemetric radio frequency signal generator, and a plurality of mol. probes, all contained on a single integrated circuit, or "biochip". The biochip is suitable for multi-gene anal., and multi-**peptide** detection, as well as simultaneous detection and quantitation of polynucleotide and **polypeptide** species using a single biochip device. Also disclosed are methods that permit rapid, large-scale, and cost-effective production of such biochip devices, as well as their use in the detection and quantitation of multiple species in a single mixed biol. sample.

ST multispectral biosensor biochip app biomol

IT **Biotechnology**
(**biochips**; multifunctional and multispectral biosensor devices and methods of use)

IT Receptors
RL: ARG (Analytical reagent use); DEV (Device component use); PEP (Physical, engineering or chemical process); PRP (Properties); ANST (Analytical study); PROC (Process); USES (Uses)
(cell; multifunctional and multispectral biosensor devices and methods of use)

IT Test kits
(detection; multifunctional and multispectral biosensor devices and methods of use)

IT Microorganism
(eukaryotic; multifunctional and multispectral biosensor devices and methods of use)

IT Lasers
(excitation micro-; multifunctional and multispectral biosensor devices and methods of use)

IT IR sources
(far-IR; multifunctional and multispectral biosensor devices and methods of use)

IT UV radiation
(far-UV; multifunctional and multispectral biosensor devices and methods of use)

IT Optical detectors
(fluorescence; multifunctional and multispectral biosensor devices and methods of use)

IT Proteins, specific or class
RL: ARG (Analytical reagent use); DEV (Device component use); PEP (Physical, engineering or chemical process); PRP (Properties); ANST (Analytical study); PROC (Process); USES (Uses)
(green fluorescent; multifunctional and multispectral biosensor devices and methods of use)

IT Cell
(intact biol.; multifunctional and multispectral biosensor devices and methods of use)

IT Filters
(low-pass; multifunctional and multispectral biosensor devices and methods of use)

IT Scattering
(luminescence; multifunctional and multispectral biosensor devices and methods of use)

IT **Computers**
(microprocessors; multifunctional and multispectral biosensor devices and methods of use)

IT Probes (nucleic acid)
RL: ARG (Analytical reagent use); DEV (Device component use); PEP (Physical, engineering or chemical process); PRP (Properties); ANST (Analytical study); PROC (Process); USES (Uses)
(mol.; multifunctional and multispectral biosensor devices and methods of use)

IT AIDS (disease)
Analytical apparatus
Animal tissue
Avalanche photodiodes
Bacteria (Eubacteria)
Biosensors
Blood analysis
Electroluminescent devices
Electromagnetic wave
Fluorescent dyes
Fluorometry

Fungi
Human immunodeficiency virus 1
IR absorption
IR sources
Immobilization, biochemical
Integrated circuits
Lasers
Lenses
Light sources
Membranes, nonbiological
Microwave
Molecular recognition
Nucleic acid hybridization
Optical amplifiers
Optical detectors
Optical filters
PCR (polymerase chain reaction)
Photodiodes
Phototransistors
UV absorption
UV sources
Virus
X-ray
(multifunctional and multispectral biosensor devices and methods of use)

IT DNA
Peptide nucleic acids
Peptides, analysis
Polynucleotides
Proteins, general, analysis
RNA
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(multifunctional and multispectral biosensor devices and methods of use)

IT **Antibodies**
Biopolymers
Chemoreceptors
Enzymes, uses
RL: ARG (Analytical reagent use); DEV (Device component use); PEP (Physical, engineering or chemical process); PRP (Properties); ANST (Analytical study); PROC (Process); USES (Uses)
(multifunctional and multispectral biosensor devices and methods of use)

IT Oligonucleotides
RL: SPN (Synthetic preparation); PREP (Preparation)
(multifunctional and multispectral biosensor devices and methods of use)

IT IR sources
(near-; multifunctional and multispectral biosensor devices and methods of use)

IT UV radiation
(near-UV; multifunctional and multispectral biosensor devices and methods of use)

IT Waveguides
(sampling; multifunctional and multispectral biosensor devices and methods of use)

IT Liquid chromatographic detectors
(spectrometric; multifunctional and multispectral biosensor devices and methods of use)

IT 9001-78-9, Alkaline phosphatase 9029-46-3, Catechol-2,3-dioxygenase 9031-11-2, β-Galactosidase
RL: ARG (Analytical reagent use); DEV (Device component use); PEP

(Physical, engineering or chemical process); PRP (Properties); ANST (Analytical study); PROC (Process); USES (Uses)
(multifunctional and multispectral biosensor devices and methods of use)

IT 286448-15-5, 1: PN: US6093568 PAGE: 76 unclaimed DNA 286448-16-6, 2: PN: US6093568 PAGE: 76 unclaimed DNA
RL: PRP (Properties)
(unclaimed nucleotide sequence; multifunctional and multispectral biosensor devices, production and methods of use)

=> => d all tot

L95 ANSWER 1 OF 7 HCAPLUS COPYRIGHT 2003 ACS on STN
AN 2000:291087 HCAPLUS
DN 132:320933
TI Antigenic epitopes with Lym-1 reactivity and uses thereof
IN Rose, Larry M.; Meares, Claude F.; O'donnell, Robert T.
PA The Regents of the University of California, USA
SO PCT Int. Appl., 40 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C07K014-705
ICS C12Q001-68; A61K039-00
CC 15-2 (Immunochemistry)
Section cross-reference(s): 3, 9
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000024777	A1	20000504	WO 1999-US23609	19991012 <--
W: AU, CA, JP, KR, NO				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 6217871	B1	20010417	US 1998-181896	19981028
US 2001019828	A1	20010906	US 2001-832510	20010410
PRAI US 1998-181896	A	19981028		

OS MARPAT 132:320933
AB This invention provides novel peptide epitopes recognized by the non-Hodgkin's B cell lymphoma reactive Lym-1 antibody. These novel peptide epitopes are capable of generating antibodies directed against Lym-1 peptide epitope expressing B-NHL cells. This invention is also directed to the treatment of B-NHL.
ST monoclonal antibody Lym1 nonHodgkin B lymphoma; MHC HLA DR B lymphoma leukemia
IT Immunoglobulins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(G2a, Lym-1; antigenic epitopes with Lym-1 reactivity for diagnosis and treatment of non-Hodgkin's B cell lymphomas)
IT Histocompatibility antigens
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(HLA-DR, HLA-DR10; antigenic epitopes with Lym-1 reactivity for diagnosis and treatment of non-Hodgkin's B cell lymphomas)
IT Histocompatibility antigens
RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(MHC (major histocompatibility complex), class II, epitope; antigenic epitopes with Lym-1 reactivity for diagnosis and treatment of non-Hodgkin's B cell lymphomas)
IT Histocompatibility antigens
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(MHC (major histocompatibility complex); antigenic epitopes with Lym-1 reactivity for diagnosis and treatment of non-Hodgkin's B cell

lymphomas)
IT Gene, animal
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(Mhc; antigenic epitopes with Lym-1 reactivity for diagnosis and treatment of non-Hodgkin's B cell lymphomas)
IT Animal cell line
(Raji; antigenic epitopes with Lym-1 reactivity for diagnosis and treatment of non-Hodgkin's B cell lymphomas)
IT Immunostimulants
(adjuvants; antigenic epitopes with Lym-1 reactivity for diagnosis and treatment of non-Hodgkin's B cell lymphomas)
IT Blood analysis
Body fluid
Epitopes
Mouse
Multiple myeloma
Nucleic acid library
Phage display library
Rabbit
Vaccines
(antigenic epitopes with Lym-1 reactivity for diagnosis and treatment of non-Hodgkin's B cell lymphomas)
IT Nucleic acids
RL: ANT (Analyte); BSU (Biological study, unclassified); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(antigenic epitopes with Lym-1 reactivity for diagnosis and treatment of non-Hodgkin's B cell lymphomas)
IT Antigens
RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antigenic epitopes with Lym-1 reactivity for diagnosis and treatment of non-Hodgkin's B cell lymphomas)
IT Leukemia
(chronic B-lymphocytic; antigenic epitopes with Lym-1 reactivity for diagnosis and treatment of non-Hodgkin's B cell lymphomas)
IT Test kits
(diagnostic; antigenic epitopes with Lym-1 reactivity for diagnosis and treatment of non-Hodgkin's B cell lymphomas)
IT Mammal (Mammalia)
(human; antigenic epitopes with Lym-1 reactivity for diagnosis and treatment of non-Hodgkin's B cell lymphomas)
IT Diagnosis
(immunodiagnosis; antigenic epitopes with Lym-1 reactivity for diagnosis and treatment of non-Hodgkin's B cell lymphomas)
IT Spleen, disease
(lymphoma with villous lymphocyte; antigenic epitopes with Lym-1 reactivity for diagnosis and treatment of non-Hodgkin's B cell lymphomas)
IT Antibodies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(monoclonal, Lym-1; antigenic epitopes with Lym-1 reactivity for diagnosis and treatment of non-Hodgkin's B cell lymphomas)
IT Lymphoma
(mucosa-associated lymphoid tissue; antigenic epitopes with Lym-1 reactivity for diagnosis and treatment of non-Hodgkin's B cell lymphomas)
IT Lymphoma
(nodular; antigenic epitopes with Lym-1 reactivity for diagnosis and treatment of non-Hodgkin's B cell lymphomas)
IT Lymphoma
(non-Hodgkin's, B cell; antigenic epitopes with Lym-1 reactivity for diagnosis and treatment of non-Hodgkin's B cell lymphomas)
IT Lymphoma

(non-Hodgkin's, mantle cell; antigenic epitopes with Lym-1 reactivity for diagnosis and treatment of non-Hodgkin's B cell lymphomas)
IT B cell (lymphocyte)
(sample; antigenic epitopes with Lym-1 reactivity for diagnosis and treatment of non-Hodgkin's B cell lymphomas)
IT Lymphoma
(splenic with villous lymphocytes; antigenic epitopes with Lym-1 reactivity for diagnosis and treatment of non-Hodgkin's B cell lymphomas)
RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
(1) Baxter-Lowe, L; US 5468611 A 1995 HCAPLUS
(2) Denardo, G; CANCER BIOTHERAPY & RADIOPHARMACEUTICALS 1998, V13(4), P231
(3) Gjertsen, M; VOX SANGUINIS 1998, V74(2), P489
(4) Harris, P; J IMMUNOL 1992, V148(7), P2169 HCAPLUS
(5) Rose, L; MOL IMMUNOL 1999, V36, P789 HCAPLUS
(6) The Trustees Of The Columbia University In The City Of New York; WO 9738310 A 1997, P10 HCAPLUS

L95 ANSWER 2 OF 7 HCAPLUS COPYRIGHT 2003 ACS on STN
AN 1999:795988 HCAPLUS
DN 132:32913
TI Methods of diagnosing renal salt wasting syndrome and Alzheimer's disease and methods of treatment
IN Maesaka, John K.
PA Winthrop-University Hospital, USA
SO PCT Int. Appl., 66 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C12Q001-25
CC 9-2 (Biochemical Methods)
Section cross-reference(s): 1
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9964621	A1	19991216	WO 1999-US13135	19990610 <--
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	US 2001021508	A1	20010913	US 1998-96335	19980611
	US 6458549	B2	20021001		
	CA 2334892	AA	19991216	CA 1999-2334892	19990610
	AU 9945602	A1	19991230	AU 1999-45602	19990610
	EP 1109929	A1	20010627	EP 1999-928559	19990610
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	US 2002197652	A1	20021226	US 2002-180712	20020625
PRAI	US 1998-96335	A	19980611		
	WO 1999-US13135	W	19990610		

AB A method is described to diagnose (1) renal salt wasting syndrome and (2) Alzheimer's disease among dementia patients by measuring a patient's level of prostaglandin D2 synthase. Methods are also described to (1) treat renal salt wasting syndrome, (2) inhibit the rate of apoptosis or (3) prevent the onset of, or slow the rate of, progression of Alzheimer's disease. These methods involve inhibiting the rate of Δ12-prostaglandin J2 synthesis or by inhibiting the activity of Δ12-prostaglandin J2.

ST prostaglandin D2 synthase disease diagnosis treatment; renal salt wasting syndrome diagnosis prostaglandin D2 synthase; Alzheimer disease diagnosis prostaglandin D2 synthase
IT Test kits
(diagnostic; methods of diagnosing renal salt wasting syndrome and Alzheimer's disease and methods of treatment)
IT Immunoassay
(immunoblotting; methods of diagnosing renal salt wasting syndrome and Alzheimer's disease and methods of treatment)
IT Immunoassay
(immunopptn.; methods of diagnosing renal salt wasting syndrome and Alzheimer's disease and methods of treatment)
IT Apoptosis
(inhibition; methods of diagnosing renal salt wasting syndrome and Alzheimer's disease and methods of treatment)
IT Alzheimer's disease
Blood analysis
Diagnosis
Urine analysis
(methods of diagnosing renal salt wasting syndrome and Alzheimer's disease and methods of treatment)
IT Antibodies
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(methods of diagnosing renal salt wasting syndrome and Alzheimer's disease and methods of treatment)
IT Kidney, disease
(renal salt wasting syndrome; methods of diagnosing renal salt wasting syndrome and Alzheimer's disease and methods of treatment)
IT 65802-85-9, Prostaglandin D2 synthase 87893-54-7, Δ12-Prostaglandin J2
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(methods of diagnosing renal salt wasting syndrome and Alzheimer's disease and methods of treatment)
RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
(1) Falls, W; Virginia Medical 1978, V105, P61
(2) Khalil Abdel-Al, Y; Pediatrics International 1999, V41, P299
(3) Maesaka, J; Am J of Kidney Diseases 1998, V32(6), P917 HCAPLUS
(4) Melegos, D; Clinical Chemistry 1996, V42(12), P1984 HCAPLUS

L95 ANSWER 3 OF 7 HCAPLUS COPYRIGHT 2003 ACS on STN
AN 1995:420445 HCAPLUS
DN 122:182768
TI Assay for protein YKL-40 as a marker for degradation of mammalian connective tissue matrixes
IN Price, Paul A.; Johansen, Julia S.
PA Regents of the University of California, USA
SO PCT Int. Appl., 52 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM G01N033-574
ICS G01N033-53; C07K015-28
CC 9-10 (Biochemical Methods)
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9502188	A1	19950119	WO 1993-US6579	19930712
	W: CA				
PRAI	WO 1993-US6579		19930712		

AB A competitive immunoassay is provided for diagnosing a disease state in a

mammal associated with degradation of connective tissue in the mammal which contains protein YKL-40. The assay can be used e.g. to identify the presence of inflammatory or degenerative joint disease and tumor metastasis (to the extent it can be correlated to serum YKL-40 levels). Serum YKL-40 levels are also suggestive of the prognosis for the length of survival in breast cancer patients following recurrence and/or metastasis of their cancers. Thus, protein YKL-40 was isolated and purified from human osteosarcoma cell line MG63 by heparin affinity chromatog. and radiolabeled with 125I or used to raise antibodies in rabbits for the immunoassay.

ST protein YKL 40 connective tissue degrdn; immunoassay protein YKL 40; antibody protein YKL 40

IT Proteins, specific or class
RL: ANT (Analyte); ANST (Analytical study)
(YKL-40; assay for protein YKL-40 as marker for degradation of mammalian connective tissue matrixes)

IT Animal tissue
Blood analysis
Body fluid
Diagnosis
Mammal
(assay for protein YKL-40 as marker for degradation of mammalian connective tissue matrixes)

IT Antibodies
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); MFM (Metabolic formation); ANST (Analytical study); BIOL (Biological study); FORM (Formation, nonpreparative); USES (Uses)
(assay for protein YKL-40 as marker for degradation of mammalian connective tissue matrixes)

IT Immunoassay
(competitive, assay for protein YKL-40 as marker for degradation of mammalian connective tissue matrixes)

IT Connective tissue
Joint, anatomical
(disease, degeneration, diagnosis; assay for protein YKL-40 as marker for degradation of mammalian connective tissue matrixes)

IT Joint, anatomical
(disease, inflammation, diagnosis; assay for protein YKL-40 as marker for degradation of mammalian connective tissue matrixes)

IT Neoplasm
(metastasis, diagnosis; assay for protein YKL-40 as marker for degradation of mammalian connective tissue matrixes)

IT Antibodies
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); MFM (Metabolic formation); ANST (Analytical study); BIOL (Biological study); FORM (Formation, nonpreparative); USES (Uses)
(monoclonal, assay for protein YKL-40 as marker for degradation of mammalian connective tissue matrixes)

IT Mammary gland
(neoplasm, prognosis; assay for protein YKL-40 as marker for degradation of mammalian connective tissue matrixes)

L95 ANSWER 4 OF 7 HCAPLUS COPYRIGHT 2003 ACS on STN
AN 1994:161635 HCAPLUS
DN 120:161635
TI Monoclonal antibodies to human glycoprotein P
IN **Cianfriglia, Maurizio**
PA Istituto Superiore di Sanita', Italy
SO PCT Int. Appl., 26 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C12P021-08

ICS C12N005-20; G01N033-574; G01N033-577; A61K039-395
CC 15-3 (Immunochemistry)
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9325700	A1	19931223	WO 1993-EP1533	19930616 <--
	W: AU, BB, BG, BR, CA, CZ, FI, HU, JP, KP, KR, LK, MG, MN, MW, NO, NZ, PL, RO, RU, SD, SK, UA, US				
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	AU 9343266	A1	19940104	AU 1993-43266	19930616
	AU 672798	B2	19961017		
	EP 648276	A1	19950419	EP 1993-912996	19930616
	EP 648276	B1	19981223		
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, NL, PT, SE				
	HU 70469	A2	19951030	HU 1994-3614	19930616
	HU 216877	B	19990928		
	JP 08501925	T2	19960305	JP 1993-501138	19930616
	AT 174967	E	19990115	AT 1993-912996	19930616
	RU 2126836	C1	19990227	RU 1994-46414	19930616
	CZ 284847	B6	19990317	CZ 1994-3181	19930616
	ES 2130271	T3	19990701	ES 1993-912996	19930616
	SK 280272	B6	19991008	SK 1994-1554	19930616
	FI 9405865	A	19950208	FI 1994-5865	19941213
	US 5766946	A	19980616	US 1994-356272	19941215
	NO 9404887	A	19941216	NO 1994-4887	19941216
PRAI	IT 1992-RM457	A	19920617		
	WO 1993-EP1533	A	19930616		

AB A monoclonal antibody that recognizes a structurally continuous extracellular epitope of the fourth extracellular loop of human glycoprotein P (Pgp) is prepared The antibodies bind human Pgp specifically and with high avidity and thus may be used to identify human MDR cells when present as only a very low proportion of a cell population or when expressing human Pgp at only very low levels. The monoclonal antibody may be a whole antibody or antigen binding fragment thereof and may be prepared by hybridoma or recombinant DNA techniques. The monoclonal antibody is useful for the identification or purification of cells which express human Pgp, e.g. when contained in heterogeneous cell populations, and for monitoring the multi-drug resistant status of cells, e.g. tumor cells. Hybridoma cells were prepared using splenocytes immunized with the lymphoblastoid T-cell line CEM-VBL100. The antibody was specific for the human MDR1 protein and did not bind to human MDR3 or mouse MDR2 or hamster MDR protein and the antibody has substantially higher affinity for MDR cell lines than prior art mAbs.

ST glycoprotein P monoclonal antibody; multidrug resistance phenotype monoclonal antibody

IT Protein sequences
(of monoclonal antibody to human glycoprotein P complementarity-determining region of mouse)

IT Glycophosphoproteins
RL: BIOL (Biological study)
(P-, gene mdr1, monoclonal antibodies to, in identification of multiple drug resistance phenotype)

IT Deoxyribonucleic acid sequences
(complementary, for monoclonal antibody to human glycoprotein P complementarity-determining region of mouse)

IT Antibodies
RL: BIOL (Biological study)
(monoclonal, to glycoprotein P, in identification of multiple drug resistance phenotype)

IT Drug resistance
(multi-, detection and treatment in human cell populations of, monoclonal antibodies to glycoprotein P for)

IT 153485-32-6
RL: PRP (Properties)
(amino acid sequence of)
IT 153314-28-4 153314-29-5
RL: PRP (Properties)
(amino acid sequence of, monoclonal antibodies recognizing, detection mdr phenotype in relation to)
IT 153485-31-5
RL: PRP (Properties)
(nucleotide sequence of)

L95 ANSWER 5 OF 7 HCAPLUS COPYRIGHT 2003 ACS on STN
AN 1993:469989 HCAPLUS
DN 119:69989
TI ADEPT: a computer program for prediction of protein antigenic determinants
AU **Maksyutov, A. Z.**; Zagrebelnaya, E. S.
CS Dep. Math. Modell., Inst. Mol. Biol., Russia, Koltsovo, 633159, Russia
SO CABIOS, Computer Applications in the Biosciences (**1993**), **9**(3), **291**-7
CODEN: COABER; ISSN: 0266-7061
DT Journal
LA English
CC 15-2 (Immunochemistry)
AB ADEPT, a program that can be used for prediction of protein antigenic determinants from the amino acid sequence alone for the cases of humoral and cellular immune response, is described. Most methods presently utilized for this purpose are implemented in the program along with some original parameters for the case of humoral immune response. There is also a possibility to combine several methods for the case of humoral immune response, which provides a means to create new predictive methods. ADEPT also includes a literature-derived database of proteins in the SWISS-PROT standard with exptl. determined antigenic determinants, so the predictive ability of new methods can be assessed within the program and corresponding statistical information is calculated ADEPT may be useful for solving various tasks involving the delineation of antigenic regions on proteins or characterization of peptide fragments, arising, for example, in protein engineering (e.g. selection of protein portions most suitable for insertion of peptide sequences that are antigenically active or possessing other desired characteristics), and in particular for construction of vaccines containing B- and/or T-cell epitopes, as well as for other problems of medico-biol. research.
ST antigenic determinant prediction computer program
IT Antigens
RL: BIOL (Biological study)
(determinants, in proteins, computer program for prediction of)
IT Computer program
(for antigenic determinant prediction in proteins)

L95 ANSWER 6 OF 7 HCAPLUS COPYRIGHT 2003 ACS on STN
AN 1988:218627 HCAPLUS
DN 108:218627
TI An integrated family of amino acid sequence analysis programs
AU **Wolf, H.**; Modrow, S.; Motz, M.; Jameson, B. A.; Hermann, G.; Foertsch, B.
CS Max von Pettenkofer Inst., Munich, D-8000/2, Fed. Rep. Ger.
SO CABIOS, Computer Applications in the Biosciences (**1988**), **4**(1), **187**-91
CODEN: COABER; ISSN: 0266-7061
DT Journal
LA English
CC 9-15 (Biochemical Methods)
AB An integrated protein anal. software package is presented for the prediction of secondary structures, based on amino acid sequence data.

The program package is designed to access protein databases and data output is an easy-to-read graphic format. The program includes a novel algorithm for the prediction of antigenic sites.

ST computer program protein structure prediction; amino acid sequence protein software

IT Protein sequences
(anal. of, computer programs for, for secondary structure prediction)

IT Algorithm
(for approaching secondary structure prediction, from amino acid sequence data)

IT Computer program
(for protein secondary structure prediction from amino acid sequence data)

IT Molecular structure determination
(of proteins, computer programs for)

IT Conformation and Conformers
(of proteins, computer programs for prediction of)

IT Proteins, properties
RL: PRP (Properties)
(structure of, computer programs for prediction of)

IT Computer application
(graphics, in protein secondary structure prediction from amino acid sequence data)

IT Virus, animal
(human immunodeficiency, protein p17 of, structure of, computer programs for prediction of)

IT Proteins, specific or class
RL: PRP (Properties)
(p17, structure of, of HIV-1 virus, computer program for prediction of)

L95 ANSWER 7 OF 7 HCAPLUS COPYRIGHT 2003 ACS on STN

AN 1988:184785 HCAPLUS

DN 108:184785

TI The antigenic index: a novel algorithm for predicting antigenic determinants

AU **Jameson, B. A.**; Wolf, H.

CS Div. Biol., California Inst. Technol., Pasadena, CA, 91125, USA

SO CABIOS, Computer Applications in the Biosciences (1988), **4**(1), **181**-6
CODEN: COABER; ISSN: 0266-7061

DT Journal

LA English

CC 15-2 (Immunochemistry)

AB A computer algorithm is described which can be used to predict the topol. features of a protein directly from its primary amino acid sequence. The computer program generates values for surface accessibility parameters and combines these values with those obtained for regional backbone flexibility and predicted secondary structure. The output of this algorithm, the antigenic index, is used to create a linear surface contour profile of the protein. Because most, if not all, antigenic sites are located within surface exposed regions of a protein, the program offers a reliable means of predicting potential antigenic determinants. The ability of this program to generate accurate surface contour profiles and predict antigenic sites from the linear amino acid sequences of well-characterized proteins was tested and a strong correlation was found between the predictions of the antigenic index and known structural and biol. data.

ST antigen determinant prediction algorithm

IT Algorithm
(for antigenic determinant prediction)

IT Antigens
RL: BIOL (Biological study)
(prediction of determinants of, algorithm for)

IT Thioredoxins
RL: BIOL (Biological study)
(S2, antigenic determinants of, prediction of, algorithm for)
IT Antigens
RL: BIOL (Biological study)
(hepatitis B envelope, pre-S-region of, prediction of determinants of, algorithm for)
IT Hemerythrins
RL: BIOL (Biological study)
(myo-, antigenic determinants of, prediction of, algorithm for)

=> => fil medline
FILE 'MEDLINE' ENTERED AT 14:56:49 ON 29 OCT 2003

FILE LAST UPDATED: 28 OCT 2003 (20031028/UP). FILE COVERS 1958 TO DATE.

On April 13, 2003, MEDLINE was reloaded. See HELP RLOAD for details.

MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the MeSH 2003 vocabulary. See http://www.nlm.nih.gov/mesh/changes2003.html for a description on changes.

This file contains CAS Registry Numbers for easy and accurate substance identification.

=> d l114 all tot

L114 ANSWER 1 OF 11 MEDLINE on STN
AN **2003060541** MEDLINE
DN **22458415** PubMed ID: **12570753**
TI Design and peptide-based validation of phage display antibodies for proteomic biochips.
AU Stich N; van Steen G; Schalkhammer T
CS Kluyver Laboratory for biotechnology, TU-Delft, Julianalaan 67, 2628BC Delft, The Netherlands.
SO COMBINATORIAL CHEMISTRY & HIGH THROUGHPUT SCREENING, (2003 Feb) 6 (1) 67-78.
Journal code: 9810948. ISSN: 1386-2073.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200303
ED Entered STN: 20030207
Last Updated on STN: 20030318
Entered Medline: 20030317
AB To validate potential application of phage display-antibody **arrays** for high-throughput screening on a novel proteomics biochip, we examined the epitopes versus the full protein of glucose-6-phosphate-dehydrogenase (G6PD) from yeast. In a predictive approach, we used the Hopp-Woods method and compared the results with antibodies directed against the entire **enzyme**. In total, 16 peptides of a length of 11 amino acids each fulfilling the desired criteria were identified and synthesized. Subsequently, antibodies against G6PD were raised using a phage display library. Selective interaction of the antibodies with certain peptides facilitated the identification of epitopes predicted by the hydropathic profile. The setup was adapted to a novel biochip system based on surface-enhanced absorption for direct CCD-camera based screening.
CT Check Tags: Animal; Support, Non-U.S. Gov't
Amino Acid Sequence
***Antibodies**

Antibody Affinity
Antibody Specificity
Enzyme-Linked Immunosorbent Assay
Epitope Mapping: MT, methods
Glucosephosphate Dehydrogenase: CH, chemistry
Glucosephosphate Dehydrogenase: IM, immunology
Microscopy, Atomic Force
Models, Molecular
Molecular Sequence Data
***Peptide Library**
***Protein Array Analysis: MT, methods**
*Proteomics: MT, methods
Saccharomyces cerevisiae: EN, enzymology
CN 0 (Antibodies); 0 (Peptide Library); EC 1.1.1.49 (Glucosephosphate Dehydrogenase)

L114 ANSWER 2 OF 11 MEDLINE on STN
AN **2003037027** MEDLINE
DN **22432643** PubMed ID: **12543931**
TI Toward a human blood serum proteome: analysis by multidimensional separation coupled with mass spectrometry.
AU Adkins Joshua N; Varnum Susan M; Auberry Kenneth J; Moore Ronald J; Angell Nicolas H; Smith Richard D; Springer David L; Pounds Joel G
CS Biological Sciences Department, Pacific Northwest National Laboratory, Richland, Washington 99352, USA.
SO Mol Cell Proteomics, (2002 Dec) 1 (12) 947-55.
Journal code: 101125647. ISSN: 1535-9476.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200309
ED Entered STN: 20030125
Last Updated on STN: 20030925
Entered Medline: 20030924
AB Blood serum is a complex body fluid that contains various proteins ranging in concentration over at least 9 orders of magnitude. Using a combination of mass spectrometry technologies with improvements in sample preparation, we have performed a proteomic analysis with submilliliter quantities of serum and increased the measurable concentration range for proteins in blood serum beyond previous reports. We have detected 490 proteins in serum by on-line reversed-phase microcapillary liquid chromatography coupled with ion trap mass spectrometry. To perform this analysis, immunoglobulins were removed from serum using protein A/G, and the remaining proteins were digested with **trypsin**. Resulting peptides were separated by strong cation exchange chromatography into distinct fractions prior to analysis. This separation resulted in a 3-5-fold increase in the number of proteins detected in an individual serum sample. With this increase in the number of proteins identified we have detected some lower abundance serum proteins (ng/ml range) including human growth hormone, interleukin-12, and prostate-specific antigen. We also used SEQUEST to compare different protein databases with and without filtering. This comparison is plotted to allow for a quick visual assessment of different databases as a subjective measure of analytical quality. With this study, we have performed the most extensive analysis of serum proteins to date and laid the foundation for future refinements in the identification of novel protein biomarkers of disease.
CT Check Tags: Female; Human
***Blood Proteins: AN, analysis**
Chromatography, High Pressure Liquid
Computational Biology
Electrophoresis, Capillary
Electrophoresis, Gel, Two-Dimensional

Peptide Mapping
***Proteome**
Spectrometry, Mass, Electrospray Ionization
Trypsin: ME, metabolism
CN 0 (Blood Proteins); 0 (Proteome); EC 3.4.21.4 (**Trypsin**)

L114 ANSWER 3 OF 11 MEDLINE on STN
AN **2003009083** MEDLINE
DN **22403307** PubMed ID: **12514928**
TI Single framework recombinant antibody fragments designed for protein chip applications.
AU Steinhauer Cornelia; Wingren Christer; Hager Ann-Christin Malmborg; Borrebaeck Carl A K
CS Department of Immunotechnology, Lund University, Lund, Sweden.
SO BIOTECHNIQUES, (2002 Dec) Suppl 38-45.
Journal code: 8306785. ISSN: 0736-6205.
CY United States
DT (EVALUATION STUDIES)
Journal; Article; (JOURNAL ARTICLE)
(VALIDATION STUDIES)
LA English
FS Priority Journals
EM 200307
ED Entered STN: 20030108
Last Updated on STN: 20030703
Entered Medline: 20030702
AB High-throughput proteomics, based on the microarray platform, requires stable, highly functional components that will yield a highly sensitive read-out of low abundance proteins. Although antibodies are the best characterized binding molecules for this purpose, only a fraction of them appear to behave satisfactorily in the chip format. Therefore, high demands need to be placed on their molecular design. In the present study, we have focused on recombinant antibody design based on a single framework for protein chip applications, aiming at defining crucial molecular probe parameters. Our results show that engineered human recombinant scFv antibody fragments that displayed appropriate biophysical properties (molecular [functional] stability in particular) can be generated, making them prime candidates for high-density antibody arrays. In fact, a superior framework that displays both multifaceted adsorption properties and very high functional stability over several months on chips (stored in a dried-out state) was identified. Taken together, designed scFv fragments based on a single molecular scaffold, readily accessible in large phage display libraries, can undoubtedly meet the requirements of probe content in antibody microarrays, particularly for global proteome analysis.
CT Check Tags: Human; Support, Non-U.S. Gov't
Antibodies, Monoclonal: CH, chemistry
Antibodies, Monoclonal: GE, genetics
Antibodies, Monoclonal: ME, metabolism
Equipment Design
Equipment Failure Analysis
***Immunoglobulin Fragments: CH, chemistry**
Immunoglobulin Fragments: GE, genetics
Immunoglobulin Fragments: ME, metabolism
Peptide Library
***Protein Array Analysis: IS, instrumentation**
Protein Array Analysis: MT, methods
Proteins: AN, analysis
***Proteins: CH, chemistry**
Proteins: GE, genetics
Proteins: ME, metabolism
Proteomics: IS, instrumentation
Proteomics: MT, methods

***Recombinant Proteins: CH, chemistry**
Recombinant Proteins: GE, genetics
Recombinant Proteins: ME, metabolism
***Sequence Analysis, Protein: IS, instrumentation**
Sequence Analysis, Protein: MT, methods
CN 0 (Antibodies, Monoclonal); 0 (Immunoglobulin Fragments); 0 (Peptide Library); 0 (Proteins); 0 (Recombinant Proteins)

L114 ANSWER 4 OF 11 MEDLINE on STN
AN **2002409637** MEDLINE
DN **22154568** PubMed ID: **12164696**
TI Adapting arrays and lab-on-a-chip technology for proteomics.
AU Figeys Daniel
CS MDS-Proteomics, Toronto, Ontario, Canada.. d.figeys@mdsp.com
SO Proteomics, (2002 Apr) 2 (4) 373-82. Ref: 29
Journal code: 101092707. ISSN: 1615-9853.
CY Germany: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 200212
ED Entered STN: 20020808
Last Updated on STN: 20021217
Entered Medline: 20021212
AB The impact of proteomics as a discovery engine in life science and in drug discovery has increased tremendously over the last seven years. At the same time, proteomics has expanded from the initial trust as a two-dimensional gel based approach to cover more functional and structural properties of proteins. The development of lab-on-a-chip and protein arrays for proteomics will have to evolve with the changes in proteomics to stay relevant. Here, we review the changes in the field of proteomics and their impact on the development in protein arrays and lab-on-a-chip.
CT **Antibodies**
Electrophoresis, Gel, Two-Dimensional: MT, methods
***Protein Array Analysis**
***Proteins: AN, analysis**
Proteins: CH, chemistry
*Proteomics
Proteomics: IS, instrumentation
Proteomics: MT, methods
Sequence Analysis, Protein
Spectrum Analysis, Mass: IS, instrumentation
Spectrum Analysis, Mass: MT, methods
CN 0 (Antibodies); 0 (Proteins)

L114 ANSWER 5 OF 11 MEDLINE on STN
AN **2002376054** MEDLINE
DN **22117022** PubMed ID: **12121125**
TI Peptide **arrays** for highly sensitive and specific antibody-binding fluorescence assays.
AU Melnyk Oleg; Duburcq Xavier; Olivier Christophe; Urbes Florence; Auriault Claude; Gras-Masse Helene
CS UMR CNRS 8525, Biological Institute of Lille, 1 rue du Pr Calmette, 59021 Lille, France.. oleg.melnyk@pasteur-lille.fr
SO BIOCONJUGATE CHEMISTRY, (2002 Jul-Aug) 13 (4) 713-20.
Journal code: 9010319. ISSN: 1043-1802.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200308

ED Entered STN: 20020718
Last Updated on STN: 20021212
Entered Medline: 20030805

AB We report a novel generation of peptide **arrays** fabricated by site-specific ligation of glyoxylyl peptides onto glass slides covered by a semicarbazide sol-gel layer. These **arrays** allowed the highly sensitive and specific detection of antibodies in very small blood samples from infected individuals using three model peptidic epitopes (HCV Core and NS4, EBV Capsid) in an immunofluorescence assay. Comparison with standard **enzyme**-linked immunosorbent assays (ELISAs) demonstrated a large gain in sensitivity and specificity. These unique properties, combined with the possibility to immobilize glycoproteins such as antibodies, offer the possibility to perform sandwich immunofluorescent assays in a highly parallel format.

CT Check Tags: Human; Support, Non-U.S. Gov't
Antibodies, Viral: BL, blood
Cross-Linking Reagents: CH, chemistry
Epitopes: CH, chemistry
Epitopes: DU, diagnostic use
Epstein-Barr Virus Infections: DI, diagnosis
*Fluoroimmunoassay: MT, methods
Fluoroimmunoassay: ST, standards
Glass
Hepatitis C: DI, diagnosis
Hepatitis C Antibodies: BL, blood
Herpesvirus 4, Human: IM, immunology
Immunologic Tests: MT, methods
Immunologic Tests: ST, standards
Microchemistry
Miniaturization
***Peptides: CS, chemical synthesis**
Peptides: DU, diagnostic use
Sensitivity and Specificity

CN 0 (Antibodies, Viral); 0 (Cross-Linking Reagents); 0 (Epitopes); 0 (Glass); 0 (Hepatitis C Antibodies); 0 (Peptides)

L114 ANSWER 6 OF 11 MEDLINE on STN
AN **2002064944** MEDLINE
DN **21650548** PubMed ID: **11790254**
TI Quoderat demonstrandum? The mystery of experimental validation of apparently erroneous computational analyses of protein sequences.
AU Iyer L M; Aravind L; Bork P; Hofmann K; Mushegian A R; Zhulin I B; Koonin E V
CS National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda, MD 20894, USA.
SO GENOMEBIOLOGY.COM, (2001) 2 (12) RESEARCH0051.
Journal code: 100960660. ISSN: 1465-6914.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200206
ED Entered STN: 20020125
Last Updated on STN: 20030105
Entered Medline: 20020614

AB BACKGROUND: Computational predictions are critical for directing the experimental study of protein functions. Therefore it is paradoxical when an apparently erroneous computational prediction seems to be supported by experiment. RESULTS: We analyzed six cases where application of novel or conventional computational methods for protein sequence and structure analysis led to non-trivial predictions that were subsequently supported by direct experiments. We show that, on all six occasions, the original prediction was unjustified, and in at least three cases, an alternative,

well-supported computational prediction, incompatible with the original one, could be derived. The most unusual cases involved the identification of an archaeal cysteinyl-tRNA synthetase, a dihydropteroate synthase and a thymidylate synthase, for which experimental verifications of apparently erroneous computational predictions were reported. Using sequence-profile analysis, multiple alignment and secondary-structure prediction, we have identified the unique archaeal 'cysteinyl-tRNA synthetase' as a homolog of extracellular polygalactosaminidases, and the 'dihydropteroate synthase' as a member of the beta-lactamase-like superfamily of metal-dependent hydrolases. CONCLUSIONS: In each of the analyzed cases, the original computational predictions could be refuted and, in some instances, alternative strongly supported predictions were obtained. The nature of the experimental evidence that appears to support these predictions remains an open question. Some of these experiments might signify discovery of extremely unusual forms of the respective **enzymes**, whereas the results of others could be due to artifacts.

CT Check Tags: Human
Acetyltransferases: CH, chemistry
Acetyltransferases: PH, physiology
Amino Acid Sequence
Amino Acyl-tRNA Ligases: CH, chemistry
Amino Acyl-tRNA Ligases: PH, physiology
Archaeal Proteins: CH, chemistry
Archaeal Proteins: PH, physiology
Artifacts
***Computational Biology**
DNA-Binding Protein, Cyclic AMP-Responsive: CH, chemistry
DNA-Binding Protein, Cyclic AMP-Responsive: PH, physiology
Dihydropteroate Synthase: CH, chemistry
Dihydropteroate Synthase: PH, physiology
Forecasting
Molecular Sequence Data
Phytochrome: CH, chemistry
Phytochrome: PH, physiology
Plant Proteins: CH, chemistry
Plant Proteins: PH, physiology
Protein Structure, Tertiary
***Proteins: CH, chemistry**
***Proteins: PH, physiology**
Sequence Alignment
***Sequence Analysis, Protein**
Thymidylate Synthase: CH, chemistry
Thymidylate Synthase: PH, physiology
Transcription Factors: CH, chemistry
Transcription Factors: PH, physiology
Viral Proteins: CH, chemistry
Viral Proteins: PH, physiology

RN 11121-56-5 (Phytochrome)
CN 0 (Archaeal Proteins); 0 (DNA-Binding Protein, Cyclic AMP-Responsive); 0 (PIF3 protein); 0 (Plant Proteins); 0 (Proteins); 0 (Transcription Factors); 0 (Viral Proteins); 0 (activating transcription factor 2 protein); 0 (movement protein, plant virus); EC 2.1.1.45 (Thymidylate Synthase); EC 2.3.1. (Acetyltransferases); EC 2.3.1.48 (histone acetyltransferase); EC 2.5.1.15 (Dihydropteroate Synthase); EC 6.1.1. (Amino Acyl-tRNA Ligases); EC 6.1.1.16 (cysteinyl-tRNA synthetase)

L114 ANSWER 7 OF 11 MEDLINE on STN
AN **2002022947** MEDLINE
DN **21358646** PubMed ID: **11464511**
TI **Array**-based ELISAs for high-throughput analysis of human cytokines.
AU Moody M D; Van Arsdell S W; Murphy K P; Orencole S F; Burns C
CS Pierce Endogen, Inc., 30 Commerce Way, Woburn, MA 01801-1059, USA..

mmoody@endogen.com
SO BIOTECHNIQUES, (2001 Jul) 31 (1) 186-90, 192-4.
Journal code: 8306785. ISSN: 0736-6205.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200112
ED Entered STN: 20020121
Last Updated on STN: 20020121
Entered Medline: 20011207
AB In this report, we describe the development of a mini-**array** system suitable for high-throughput quantification of proteins. This mini-**array** is a multiplexed, sandwich-type ELISA that measures the concentration of seven different human cytokines--TNF-alpha, IFN alpha, IFN gamma, IL-1 alpha, IL-1 beta, IL-6, and IL-10--from a single sample in each well of a 96-well plate. The mini-**array** is produced by spotting monoclonal antibodies (mAbs) in a 3 x 3 pattern in the bottom of the wells of 96-well polystyrene plates. Cytokines that are captured by the **arrayed** mAbs are detected by using biotinylated mAbs, followed by the addition of a streptavidin-horseradish peroxidase (HRP) conjugate and a chemiluminescent substrate. The light produced from the HRP-catalyzed oxidation of the substrate is measured at each spot in the **array** by imaging the entire plate with a commercially available CCD camera. Here, we demonstrate that these 96-well-plate format mini-**arrays** have performance characteristics that make them suitable for the high-throughput screening of anti-inflammatory compounds.
CT Check Tags: Human
Anti-Inflammatory Agents: PD, pharmacology
Antibodies, Monoclonal
Cell Line
*Cytokines: AN, analysis
Cytokines: IM, immunology
***Enzyme-Linked Immunosorbent Assay: MT, methods**
Interferon Type II: AN, analysis
Interferon Type II: IM, immunology
Interferon-alpha: AN, analysis
Interferon-alpha: IM, immunology
Interleukin-1: AN, analysis
Interleukin-1: IM, immunology
Interleukin-10: AN, analysis
Interleukin-10: IM, immunology
Interleukin-6: AN, analysis
Interleukin-6: IM, immunology
Monocytes: CY, cytology
Monocytes: DE, drug effects
Monocytes: IM, immunology
Sensitivity and Specificity
Tumor Necrosis Factor: AN, analysis
Tumor Necrosis Factor: IM, immunology
RN 130068-27-8 (Interleukin-10); 82115-62-6 (Interferon Type II)
CN 0 (Anti-Inflammatory Agents); 0 (Antibodies, Monoclonal); 0 (Cytokines); 0 (Interferon-alpha); 0 (Interleukin-1); 0 (Interleukin-6); 0 (Tumor Necrosis Factor)

L114 ANSWER 8 OF 11 MEDLINE on STN
AN **2002009902** MEDLINE
DN **21254788** PubMed ID: **11355348**
TI Protein chips based on recombinant antibody fragments: a highly sensitive approach as detected by mass spectrometry.
AU Borrebaeck C A; Ekstrom S; Hager A C; Nilsson J; Laurell T; Marko-Varga G
CS Lund University, Lund, Sweden.. carl.borrebaeck@immun.lth.se

SO BIOTECHNIQUES, (2001 May) 30 (5) 1126-30, 1132.
Journal code: 8306785. ISSN: 0736-6205.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200112
ED Entered STN: 20020121
Last Updated on STN: 20020121
Entered Medline: 20011204
AB With the human genome in a first sequence draft and several other genomes being finished this year, the existing information gap between genomics and proteomics is becoming increasingly evident. The analysis of the proteome is, however, much more complicated because the synthesis and structural requirements of functional proteins are different from the easily handled oligonucleotides, for which a first analytical breakthrough already has come in the use of DNA chips. In comparison with the DNA **microarrays**, the protein **arrays**, or protein chips, offer the distinct possibility of developing a rapid global analysis of the entire proteome. Thus, the concept of comparing proteomic maps of healthy and diseased cells may allow us to understand cell signaling and metabolic pathways and will form a novel base for pharmaceutical companies to develop future therapeutics much more rapidly. This report demonstrates the possibilities of designing protein chips based on specially constructed, small recombinant antibody fragments using nano-structure surfaces with biocompatible characteristics, resulting in sensitive detection in the 600-amol range. The assay readout allows the determination of single or multiple antigen-antibody interactions. Mass identity of the antigens, currently with a resolution of 8000, enables the detection of structural modifications of single proteins.
CT Check Tags: Comparative Study; Support, Non-U.S. Gov't
***Antibodies**
Cholera Toxin: IM, immunology
Immunoglobulin Variable Region
Oligonucleotide Array Sequence Analysis
***Peptide Fragments**
Proteins: AN, analysis
*Proteins: CH, chemistry
Proteins: IM, immunology
*Recombinant Proteins
Spectrometry, Mass, Matrix-Assisted Laser Desorption-Ionization
*Spectrum Analysis, Mass
RN 9012-63-9 (Cholera Toxin)
CN 0 (Antibodies); 0 (Immunoglobulin Variable Region); 0 (Peptide Fragments); 0 (Proteins); 0 (Recombinant Proteins)

L114 ANSWER 9 OF 11 MEDLINE on STN
AN **2001010196** MEDLINE
DN **20429628** PubMed ID: **10973222**
TI Antibody **arrays** for high-throughput screening of antibody-antigen interactions.
CM Comment in: Nat Biotechnol. 2000 Sep;18(9):932-3
AU de Wildt R M; Mundy C R; Gorick B D; Tomlinson I M
CS MRC Laboratory of Molecular Biology and MRC Centre for Protein Engineering, Hills Road, Cambridge CB2 2QH, UK.. rdw@mrc-lmb.cam.ac.uk
SO NATURE BIOTECHNOLOGY, (2000 Sep) 18 (9) 989-94.
Journal code: 9604648. ISSN: 1087-0156.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200010
ED Entered STN: 20010322

Last Updated on STN: 20010322
Entered Medline: 20001023

AB We have developed a novel technique for high-throughput screening of recombinant antibodies, based on the creation of antibody **arrays**. Our method uses robotic picking and high-density gridding of bacteria containing antibody genes followed by filter-based **enzyme**-linked immunosorbent assay (ELISA) screening to identify clones that express binding antibody fragments. By eliminating the need for liquid handling, we can thereby screen up to 18,342 different antibody clones at a time and, because the clones are **arrayed** from master stocks, the same antibodies can be double spotted and screened simultaneously against 15 different antigens. We have used our technique in several different applications, including isolating antibodies against impure proteins and complex antigens, where several rounds of phage display often fail. Our results indicate that antibody **arrays** can be used to identify differentially expressed proteins.

CT Check Tags: Human
Amino Acid Sequence
***Antibodies: CH, chemistry**
*Antigen-Antibody Reactions
Bacteria: CH, chemistry
Bacteria: GE, genetics
Biochemistry: MT, methods
*Biosensing Techniques: MT, methods
Blotting, Western
Enzyme-Linked Immunosorbent Assay
Hela Cells
Molecular Probe Techniques
Molecular Sequence Data
***Oligonucleotide Array Sequence Analysis**
Peptide Library
Protein Conformation
*Proteins: CH, chemistry
Proteins: ME, metabolism
Recombinant Proteins: CH, chemistry
Robotics
Serum Albumin: CH, chemistry
Serum Albumin, Bovine: CH, chemistry

CN 0 (Antibodies); 0 (Peptide Library); 0 (Proteins); 0 (Recombinant Proteins); 0 (Serum Albumin); 0 (Serum Albumin, Bovine)

L114 ANSWER 10 OF 11 MEDLINE on STN
AN **2000230098** MEDLINE
DN **20230098** PubMed ID: **10764605**
TI Antibodies and immunoassays.
AU Madersbacher S; Berger P
CS Institute for Biomedical Aging Research, Austrian Academy of Sciences, Innsbruck, Austria.
SO METHODS, (2000 May) 21 (1) 41-50.
Journal code: 9426302. ISSN: 1046-2023.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200005
ED Entered STN: 20000606
Last Updated on STN: 20000606
Entered Medline: 20000523

AB As a glycoprotein hormone, human chorionic gonadotropin (hCG) is not a single molecular entity. This term comprises not only the bioactive heterodimer hCG but also an **array** of molecular protein backbone and glycosylation variants, such as its free beta (hCGbeta) and alpha (hCGalpha) subunits and clipped, cleaved, terminally differently

sialylated, and overglycosylated forms. This heterogeneity places great demands on selective detection systems for hCG-derived molecules. Measurement of hCG and/or its derivatives is highly dependent on the selection of target molecules and the natural variability of hCG in the specimens analyzed. Monoclonal antibody (mAb)-based immunoassays are still the state-of-the-art technique for both clinical and research applications but a major problem is the different extents of recognition of hCG variants by mAbs used in different immunoassays. On the whole, construction of sandwich-type assays obviously must take into consideration mAb characteristics, such as main and fine specificities, cross-reactivities, epitope locations and compatibilities, overlap and overhang in specificities (pairs of mAbs), and, finally, overspecificity. Consequences of overhang and overlap in antigen recognition of coating and detection mAb specificities are nondesirable assay cross-reactions and competitive interference by antigenic variants. The general agreement on the most favorable assay design is contrasted by the variety of isotopic and nonisotopic detection systems in current use. The **immunoenzymometric** assay (IEMA) technique is hampered by a relatively small measuring range and limited sensitivity. By measuring substrate absorption values off the absorption maximum, the measuring range of any IEMA can be extended significantly, as shown for 3,3',5,5'-tetramethylbenzidine (TMB), without jeopardizing assay characteristics. Sensitivity of the IEMA can be enhanced by modifying the horseradish peroxidase (HRPO) labeling technique by using highly purified mAb preparations and higher-input HRPO/mAb ratios. We have also compared the assay characteristics of time-resolved fluoroimmunoassay (IFMA), IEMA, immunoradiometric assay (IRMA), and competitive radioimmunoassay (RIA) based on identical mAbs. Reasons for the observed superiority of the IFMA lie in its concept of signal detection and the high specific labeling of the detection mAb which on a molar basis can be up to 7-fold and 15-fold higher compared with (125)I and HRPO, respectively.

CT Check Tags: Human; Support, Non-U.S. Gov't
***Antibodies, Monoclonal: CH, chemistry**
Antibody Specificity
Chorionic Gonadotropin: CH, chemistry
Chorionic Gonadotropin: IM, immunology
Chromatography, High Pressure Liquid
Dose-Response Relationship, Drug
Durapatite: CH, chemistry
***Enzyme-Linked Immunosorbent Assay: MT, methods**
Epitopes
Europium: CH, chemistry
*Gonadotropins: CH, chemistry
Gonadotropins: IM, immunology
*Immunoassay: MT, methods
Immunoassay: TD, trends
Protein Isoforms
Sensitivity and Specificity
Time Factors
RN 1306-06-5 (Durapatite); 7440-53-1 (Europium)
CN 0 (Antibodies, Monoclonal); 0 (Chorionic Gonadotropin); 0 (Epitopes); 0 (Gonadotropins); 0 (Protein Isoforms)

L114 ANSWER 11 OF 11 MEDLINE on STN
AN **2000129619** MEDLINE
DN **20129619** PubMed ID: **10662483**
TI Recent progress in biomolecular engineering.
AU Ryu D D; Nam D H
CS Biochemical Engineering Program, University of California, Davis, California 95616, USA.. DDYRYU@UCDAVIS.EDU
SO BIOTECHNOLOGY PROGRESS, (2000 Jan-Feb) 16 (1) 2-16. Ref: 172
Journal code: 8506292. ISSN: 8756-7938.

CY United States
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, ACADEMIC)
LA English
FS Priority Journals
EM 200003
ED Entered STN: 20000330
Last Updated on STN: 20000330
Entered Medline: 20000320

AB During the next decade or so, there will be significant and impressive advances in biomolecular engineering, especially in our understanding of the biological roles of various biomolecules inside the cell. The advances in high throughput screening technology for discovery of target molecules and the accumulation of functional genomics and proteomics data at accelerating rates will enable us to design and discover novel biomolecules and proteins on a rational basis in diverse areas of pharmaceutical, agricultural, industrial, and environmental applications. As an applied molecular evolution technology, DNA shuffling will play a key role in biomolecular engineering. In contrast to the point mutation techniques, DNA shuffling exchanges large functional domains of sequences to search for the best candidate molecule, thus mimicking and accelerating the process of sexual recombination in the evolution of life. The phage-display system of combinatorial peptide libraries will be extensively exploited to design and create many novel proteins, as a result of the relative ease of screening and identifying desirable proteins. Even though this system has so far been employed mainly in screening the combinatorial antibody libraries, its application will be extended further into the science of protein-receptor or protein-ligand interactions. The bioinformatics for genome and proteome analyses will contribute substantially toward ever more accelerated advances in the pharmaceutical industry. Biomolecular engineering will no doubt become one of the most important scientific disciplines, because it will enable systematic and comprehensive analyses of gene expression patterns in both normal and diseased cells, as well as the discovery of many new high-value molecules. When the functional genomics database, EST and SAGE techniques, **microarray** technique, and proteome analysis by 2-dimensional gel electrophoresis or capillary electrophoresis in combination with mass spectrometer are all put to good use, biomolecular engineering research will yield new drug discoveries, improved therapies, and significantly improved or new bioprocess technology. With the advances in biomolecular engineering, the rate of finding new high-value peptides or proteins, including antibodies, vaccines, **enzymes**, and therapeutic peptides, will continue to accelerate. The targets for the rational design of biomolecules will be broad, diverse, and complex, but many application goals can be achieved through the expansion of knowledge based on biomolecules and their roles and functions in cells and tissues. Some engineered biomolecules, including humanized Mab's, have already entered the clinical trials for therapeutic uses. Early results of the trials and their efficacy are positive and encouraging. Among them, Herceptin, a humanized Mab for breast cancer treatment, became the first drug designed by a biomolecular engineering approach and was approved by the FDA. Soon, new therapeutic drugs and high-value biomolecules will be designed and produced by biomolecular engineering for the treatment or prevention of not-so-easily cured diseases such as cancers, genetic diseases, age-related diseases, and other metabolic diseases. Many more industrial **enzymes**, which will be engineered to confer desirable properties for the process improvement and manufacturing of high-value biomolecular products at a lower production cost, are also anticipated. New metabolites, including novel antibiotics that are active against resistant strains, will also be produced soon by recombinant organisms having de novo engineered biosynthetic pathway **enzyme** systems. The biomolecular engineering era is here, and

many of benefits will be derived from this field of scientific research for years to come if we are willing to put it to good use.

CT Check Tags: Animal; Human
Antibiotics, Peptide
Antibodies: GE, genetics
*Biomedical Engineering: TD, trends
Biotechnology: TD, trends
Computational Biology
Enzymes: GE, genetics
Genetic Engineering: TD, trends
Immunotoxins
Mutagenesis, Site-Directed
Peptide Library
Vaccines, Synthetic

CN 0 (Antibiotics, Peptide); 0 (Antibodies); 0 (**Enzymes**); 0 (Immunotoxins); 0 (Peptide Library); 0 (Vaccines, Synthetic)

=> => fil wpix
FILE 'WPIX' ENTERED AT 15:30:35 ON 29 OCT 2003
COPYRIGHT (C) 2003 THOMSON DERWENT

FILE LAST UPDATED: 27 OCT 2003 <20031027/UP>
MOST RECENT DERWENT UPDATE: 200369 <200369/DW>
DERWENT WORLD PATENTS INDEX SUBSCRIBER FILE, COVERS 1963 TO DATE

>>> NEW WEEKLY SDI FREQUENCY AVAILABLE --> see NEWS <<<

>>> SLART (Simultaneous Left and Right Truncation) is now available in the /ABEX field. An additional search field /BIX is also provided which comprises both /BI and /ABEX <<<

>>> PATENT IMAGES AVAILABLE FOR PRINT AND DISPLAY <<<

>>> FOR A COPY OF THE DERWENT WORLD PATENTS INDEX STN USER GUIDE, PLEASE VISIT:
http://www.stn-international.de/training_center/patents/stn_guide.pdf <<<

>>> FOR DETAILS OF THE PATENTS COVERED IN CURRENT UPDATES, SEE http://thomsonderwent.com/coverage/latestupdates/ <<<

>>> FOR INFORMATION ON ALL DERWENT WORLD PATENTS INDEX USER GUIDES, PLEASE VISIT:
http://thomsonderwent.com/support/userguides/ <<<

=> d all abeq tech abex tot

L155 ANSWER 1 OF 3 WPIX COPYRIGHT 2003 THOMSON DERWENT on STN
AN **2002-645691** [70] WPIX
DNN **N2002-510498** DNC **C2002-182410**
TI Generating amino acid sequences representative of desired **polypeptide**, by **computationally** generating proteolytic cleavage products, **analyzing** and selecting the set of products, thus generating amino acid sequences.
DC B04 D16 S03 **T01**
IN **KATZ, E I**
PA (KATZ-I) KATZ E I
CYC 28
PI EP 1223534 A1 20020717 (200270)* EN 124p G06F019-00 <--
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR

US 2002137119 A1 20020926 (200270) G06G007-48 <--
JP 2002360278 A 20021217 (200312) 250p C12N015-09 <--
ADT EP 1223534 A1 EP 2002-75095 20020111; US 2002137119 A1 US 2001-982172 20011019; JP 2002360278 A JP 2002-4906 20020111
PRAI US 2001-982172 20011019; IL 2001-140881 20010114
IC ICM **C12N015-09; G06F019-00; G06G007-48**
ICS **C07K001-12; C07K002-00; C07K016-18; C12M001-34; C12P021-06; C12P021-08; C12Q001-37; G01N033-53; G01N033-68; G01N037-00; G06G007-58**
AB EP 1223534 A UPAB: 20021031
NOVELTY - Generating (M1) set of amino acid sequences (AAS) representative of one desired **polypeptide** (I), involves **computationally** generating a number of proteolytic cleavage products (PCP) from (I), **analyzing** the PCP according to one parameter defining a characteristic of AAS and selecting a set of PCP according to a preset criteria for each parameter, thus generating the set of AAS representative of (I).

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a **computer** readable storage media (II) comprising a database of amino acid sequences corresponding to the **polypeptide** of interest which is generated by **computationally** generating a number of proteolytic cleavage products from at least one **polypeptide** of interest, **computationally analyzing** the number of proteolytic cleavage products according to at least one parameter defining a characteristic of an amino acid sequence and storing a sequence of each of the proteolytic cleavage products thus generating the database of amino acid sequences;

(2) a system (III) (10) for generating a database of amino acid sequences corresponding to a **polypeptide** of interest, comprises a processing unit (12) which executes a software application configured for generating the number of proteolytic cleavage products from one **polypeptide** of interest, and **analyzing** the number of proteolytic cleavage products according to one parameter defining a characteristic of amino acid sequence;

(3) a kit (K) for quantifying at least one **polypeptide** of interest, comprises a number of **peptides** or **antibodies** each capable of specifically recognizing at least one **peptide**, where the number of **peptides** is generated according to information derived from **computational analysis** of the **polypeptide** of interest, where the **computational analysis** including generating a number of proteolytic cleavage products from the **polypeptide** of interest; and

(4) quantifying (M2) one **polypeptide** of interest in a biological sample, involves contacting the biological sample with proteolytic agent, so as to obtain a proteolyzed biological sample, contacting the proteolyzed biological sample with at least one **antibody** and at least one **peptide** of a number of **peptides**, and detecting presence, absence and/or level of **antibody** binding to thus quantify one **polypeptide** of interest in the biological sample.

USE - M1 is useful for generating at least one **antibody** specific to a **polypeptide** of interest (claimed).

DESCRIPTION OF DRAWING(S) - The figure shows a system designed and configured for generating a database of amino acids sequence representative of the desired protein.

System 10

Processing unit 12

Dwg.1/4
FS CPI EPI
FA AB; GI; DCN
MC CPI: **B04-C01; B04-G01;** B04-L05C; **B04-N04;**

B05-C03; B10-A14; **B11-C07A**; **B11-C08E3**; **B11-C08F4**; B12-K04; D05-H09; D05-H10; **D05-H11**; D05-H12A; D05-H17A6
EPI: **S03-E14H**; **S03-E14H4**; **T01-J**

TECH UPTX: 20021031
TECHNOLOGY FOCUS - BIOTECHNOLOGY - Preferred Method: In M1, the number of proteolytic cleavage products are generated according to proteolytic cleavage pattern of at least one proteolytic agent. The proteolytic cleavage products are proteolytic **enzyme** (**trypsin**, **chymotrypsin**, **subtilisin**, **pepsin**, **V8 protease**, **thrombin** or **elastase**) and proteolytic chemical (**cyanogen bromide** or 2-**nitro-5-thiocyanobenzoate**). At least one parameter defining a characteristic of an amino acid sequence is selected from molecular weight, amino acid composition, hydrophobicity, hydrophilicity, charge, secondary structure, heterogeneity, length, post-translational modifications, polarity, solubility, amphipathic nature, sequence or immunogenicity. In M2, solid substrate is configured as a **microarray** and the number of **antibodies** or **peptides** are attached to the **microarray** in a region-specific manner.
Preferred Kit: In (K), **computational analysis** further includes **analysis** of the number of proteolytic cleavage products according to one parameter defining a characteristic of amino acid sequence and selection of a set of proteolytic cleavage products from the number of proteolytic cleavage products according to predetermined criteria for each of the parameter. The **peptides** or **antibodies** are labeled or attached to a solid substrate. The number of **peptides** or **antibodies** is contained in an individual container or mixed in a single container. The number of **peptides** are generated by **peptide** synthesis or proteolytic cleavage of one **polypeptide** of interest.

ABEX UPTX: 20021031
EXAMPLE - Multi-drug resistance (MDR) associated proteins in a biological sample was quantified. A cell culture which exhibits an MDR phenotype was dissolved by suspending the sample in a 1-2% sodium dodecyl sulfate (SDS). Denatured proteins were precipitated followed at 20degreesC. The protein precipitate was resuspended and **trypsin** was added to the resuspended sample. Tryptic digestion was allowed until complete proteolytic fragmentation of the sample protein. At the completion of digestion, residual tryptic activity was terminated by adding bovine **trypsin** inhibitor. Subsequently, a portion of the tryptic-digested sample was added to an **antibody** matrix. Incubation was allowed to proceed to allow formation of immunocomplexes, following which, the matrix was washed twice with phosphate buffered saline to reduce non-specific binding. Monitoring specific binding of sample proteins to the matrix was effected using a mixture of fluorescently labeled **polypeptides** against which the matrix **antibodies** were raised. The intensity of the fluorescent signal obtained from the matrix as correlated to specific positions in the matrix gave a quantitative measure of the amount of protein present in the sample, after considering the amount of protein sample applied to the matrix, and control binding, as determined using signals obtained from control **antibodies**.

L155 ANSWER 2 OF 3 WPIX COPYRIGHT 2003 THOMSON DERWENT on STN
AN **2002-025218** [03] WPIX
DNC **C2002-006935**
TI Analysis of protein or **enzyme** activity in samples, e.g., biopsies, comprises using a pool of tagged substrates which can then be sorted onto a solid surface **array** after reaction.
DC B04 D16
IN VOLINIA, S
PA (VOLI-I) VOLINIA S

CYC 1
PI US 2001031469 A1 20011018 (200203)* 36p C12Q001-68 <--
ADT US 2001031469 A1 Provisional US 2000-174171P 20000103, US 2001-753114 20010102
PRAI US 2000-174171P 20000103; US 2001-753114 20010102
IC ICM **C12Q001-68**
AB US2001031469 A UPAB: 20020114
NOVELTY - Processes for analyzing the activity or level of one or more proteins or **enzymes**, using a pool of tagged substrates, are new.

DETAILED DESCRIPTION - Analyzing (A) the activity or level of one or more proteins or **enzymes**, comprises:

(1) the method (A) of:

(a) providing a pool of substrates (e.g. **peptides**, **antibodies**, binding domains or other molecules which act as substrates or control substrates), each with a specific tag and representing a substrate of one or more of the proteins or **enzymes**, or substrates derived from these using the tagged substrates as substrates;

(b) hybridizing the pool of tagged substrates to an ordered **array** of specific and complementary tags immobilized on a surface, where the **array** comprises different tags, at least some of which are control tags, each tag is localized in a predetermined region of the surface and the density of different tags is greater than 100 different tags per cm2, and all tags in the substrates derived using the proteins or **enzymes** are complementary to at least some of the immobilized tags;

(c) quantifying hybridization of the substrates tagged with nucleic acids or **peptide** nucleic acids (PNAs) to the **array**, where the quantification is proportional to the activity of proteins or **enzymes** which modify or attach to the substrates tagged with nucleic acids or PNAs; or

(2) the method (B) of:

(a) providing a pool of molecules (e.g. **peptides**, **antibodies**, binding domains or other molecules which act as substrates or control substrates), each representing a substrate of one or more of the proteins or **enzymes**, or substrates derived from these;

(b) reacting the pool of molecules with an **array** of proteins, **peptides** or other non-DNA molecules, which are immobilized on a surface, where each protein, **peptide** or other non-DNA molecule is localized in a predetermined region of the surface and the density of these molecules is greater than 60 molecules per cm2; and

(c) quantifying the reactivity of the **array**, where the quantification is proportional to the activity of proteins or **enzymes** which modify or attach to the substrates.

USE - The processes are useful for analysis of the activity or level of proteins or **enzymes** (claimed). They can be used for detection of post-translationally modified proteins and for identifying target proteins capable of binding to, or serving as, **enzymes** or molecular adapters involved in biological functions. They can be used, e.g., for analyzing biopsies from cancers and other multifactorial diseases. They can be used to identify previously unknown proteins or new substrates.

ADVANTAGE - The use of tagged substrates rather than immobilized substrates leads to increased stability of the substrate, improved quality control and lower production costs. The tagged substrate can be kept lyophilized until use, separate from other tagged substrates. The quality of each tagged compound can be verified at any stage. Substrates can be changed, refined or differentially labelled at any time, without the need for designing or printing a new tag **array**.

Dwg.0/21
FS CPI
FA AB; DCN

MC CPI: B04-E01; B04-E05; B04-E10; **B04-G01**; B04-H01; B04-L01; **B04-N04**; B11-C07A; B11-C07A5; B11-C07B3; B11-C08E5; B11-C08E6; **B11-C08F4**; B12-K04A; B12-K04A1; B12-K04E; B12-K04F; D05-H09

TECH UPTX: 20020114

TECHNOLOGY FOCUS - BIOLOGY - Preferred Process: in (A), the pool of substrates comprises substrates tagged with nucleic acids or PNAs. The ordered **array** of specific and complementary tags immobilized on the surface comprises an ordered **array** of specific and complementary nucleic acids or PNAs immobilized on the surface. The quantification step comprises calculating the difference in hybridization signal intensity between each of the tagged substrates and its corresponding related elements. This typically comprises calculating the average difference in hybridization signal intensity between each of the tagged substrates and its corresponding control substrate for each protein or **enzyme**, where the control substrate has an identical tag or a different tag. The multiplicity of substrates tagged with a nucleic acid or PNA is 100 or more. For each protein or **enzyme**, the **array** comprises at least 8 different substrates which are tagged with a nucleic acid or a PNA. The hybridization is performed with a fluid volume of 200 microliters or less. The nucleic acid or PNA tags are at least 21 nucleotides in length. The control substrates comprise either premodified substrates or substrates which are substrates of constitutionally expressed control proteins or **enzymes**. In (B), the pool of molecules also comprises the same substrate for more than one different element in the **array**. Quantification comprises calculating the difference in signal intensity between each of the **array** elements. This typically comprises calculating the average difference in signal intensity between each of the **array** elements and its corresponding control substrate for each protein or **enzyme**. The multiplicity of **array** elements is 100 or more. The hybridization is performed with a fluid volume of 200 microliters or less. The control substrates comprise either premodified substrates or substrates which are substrates of constitutively expressed control proteins or **enzymes**. In both (A) and (B), the tagged substrates include glutathione-S-transferase (GST)-Pin1, GST-14-3-3, GSTFynSH2, GST-p85, GST-shcSH2, GST-p85, GST-ShcPTB, GST-ShcSH2 and GST-Grb2. The control substances are substrates for protein kinase C alpha, protein kinase C beta1, protein kinase C beta2 protein kinase C gamma, phosphatidylinositol 3-kinase alpha, phosphatidylinositol 3-kinase beta, phosphatidylinositol 3-kinase C2 beta, phosphatidylinositol 3-kinase C2 gamma, src, abl, or platelet-derived growth factor receptor. the pool of molecules comprises fluorescent labeled molecules. Quantifying comprises quantifying fluorescence of a label on the reacted substrate at a spatial resolution of 100 micrometers or higher.

ABEX UPTX: 20020114

EXAMPLE - In a typical process, a mix comprising a high number of different tagged substrates, e.g., one thousand or more, in solution in a buffer, was applied to a sample under investigation (e.g. a cell lysate). A labelling agent and/or specific inhibitors can be added to the reaction in order to follow a biochemical reaction or to evaluate a particular subset of **enzyme** reactions. The reaction was stopped, when complete, and the tagged substrate was purified using an affinity column, in order to separate the tagged substrates from the sample. Each tagged substrate was then sorted by hybridization onto a DNA/PNA tag **array** slide, which had been previously prepared by using an ordered matrix comprising the complementary DNA/PNA to each tag of the tagged substrates. Finally, the sorted modified substrates were **analyzed**, e.g., by fluorescence scanning. A **computer** program was used to average the different measurements from different sorted substrates.

L155 ANSWER 3 OF 3 WPIX COPYRIGHT 2003 THOMSON DERWENT on STN

AN **2000-061972** [05] WPIX
DNN **N2000-048567** DNC **C2000-017100**
TI Screening molecules for their activity, structure or function.
DC B04 D16 J04 P73 S03 **T01**
IN LEWIS, N S; VAID, T P
PA (CALY) CALIFORNIA INST OF TECHNOLOGY
CYC 21
PI WO 9953300 A1 19991021 (200005)* EN 56p G01N027-00
RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE
W: CA JP
EP 1073893 A1 20010207 (200109) EN G01N027-00
R: DE FR GB
US 6350369 B1 20020226 (200220) G01N027-26
JP 2002511581 W 20020416 (200242) 59p G01N027-12
US 2002081232 A1 20020627 (200245) C12M001-34 <--
ADT WO 9953300 A1 WO 1999-US8263 19990413; EP 1073893 A1 EP 1999-916681 19990413, WO 1999-US8263 19990413; US 6350369 B1 Provisional US 1998-81781P 19980414, US 1999-291932 19990413; JP 2002511581 W WO 1999-US8263 19990413, JP 2000-543816 19990413; US 2002081232 A1 Provisional US 1998-81781P 19980414, Cont of US 1999-291932 19990413, US 2001-17221 20011213
FDT EP 1073893 A1 Based on WO 9953300; JP 2002511581 W Based on WO 9953300
PRAI US 1998-81781P 19980414; US 1999-291932 19990413; US 2001-17221 20011213
IC ICM **C12M001-34**; G01N027-00; G01N027-12; G01N027-26
ICS B32B005-22; G01N027-02; G01N027-22
AB WO 9953300 A UPAB: 20000128
NOVELTY - A method for screening molecules for a specific activity, structure or function is new.

DETAILED DESCRIPTION - A method for screening molecules for a specific activity, structure or function, comprises:

(a) contacting differentially responsive sensors with a molecule of interest;

(b) measuring a signal output from each sensor;

(c) using the results of the measurements to obtain a signal profile, related to a change in signal output from each sensor; and

(d) comparing the signal profile to at least one previously obtained signal profile indicating a standard sample having a specific activity, structure or function. The signal profile is indicative of a specific activity, function, or structure.

INDEPENDENT CLAIMS are also included for:

(1) a method for screening molecules for a specific activity, structure or function, comprising:

(a) measuring outputs of chemically sensitive resistors, each resistor comprising a conductive material and a nonconductive material;

(b) using results of the measuring to obtain a signal profile, related to a change in resistance in the resistors; and

(c) comparing the signal profile to at least one previously obtained signal profile indicating a standard sample having a specific activity, structure or function; and

(2) a molecule screening system, comprising:

(a) a sensor **array** comprising differentially responsive sensors, having a first signal profile produced by the sensors, when contacted with a first **analyte** at a first concentration and a second different signal profile when contacted with a second **analyte**, wherein the difference between the first signal and the second signal being indicative of a property of the first **analyte** and second **analyte**;

(b) a measuring device, connected to the sensor **array**; and

(c) a **computer**.

The measuring device detecting the first and second signal in each of the sensors and the **computer** assembling the signal into a sensor **array** signal profile. The **computer** is operative to

compare the signal profile to at least one previously obtained signal profile indicating a standard sample having a specific activity, structure of function, wherein the signal profile is indicative of a specific activity, structure or function of the **analyte**.

USE - The method is useful for the screening of a molecule or an **analyte** of interest.

Dwg.0/8

FS CPI EPI GMPI

FA AB; DCN

MC CPI: B04-B01B; B04-E02; B04-E03; **B04-G01**; B04-G21; B04-G22; B04-J01; B04-L01; B04-L03B; B04-L04; B04-L05; B04-L05A; B04-L05B; B04-L05C; B04-N02; **B04-N04**; B11-C07; B11-C08; B12-K04; D05-H09; J04-B01; J04-C02

EPI: S03-E03C; S03-E04E; S03-E09E; S03-E14H4; S03-E14H5; **T01-J07A3** ; **T01-J07B**

TECH UPTX: 20000128

TECHNOLOGY FOCUS - BIOTECHNOLOGY - Preferred materials: The molecule of interest is selected from a nucleic acid (e.g. DNA or RNA), a **polypeptide** (e.g. **antibody**, **enzyme** and protein), a biochemical (e.g. lipid, hormone, fatty acids and carbohydrate and a chemical (e.g. alkanes, alkenes, alkynes, dienes, alicyclic hydrocarbons, arenes, alcohols, ethers, ketones, aldehydes, carbonyls, carbanions, polynuclear aromatics and their derivatives). The **antibody** is a monoclonal **antibody**, polygonal **antibody**, humanized **antibody**, or their fragments. The **enzyme** is selected from lipases, esterases, proteases, glycosidases, glycosyl transferases, phosphateases, kinases, mono- and dioxygenases, haloperoxidases, lignin peroxidases, diarylpropane peroxidases eposide hydrolases, nitrile hydrotasees, nitrilases, transaminases, amidases and acylases. The specific activity is selected from **enzymatic** activity, binding activity, inhibitory activity and modulating activity. The specific structure is selected from a three-dimensional structure, amino acid sequence and nucleic acid sequence. The differentially responsive sensor senses changes in optics, resonance and/or current. The differentially responsive sensor is selected crystalline colloidal **array** (CCA) containing sensors, metal oxide sensors, dye-impregnated polymers coated onto beads or optical fibers, bulk conducting organic polymers, capacitance sensors and/or chemically sensitive resistor sensors. The signal profile of the standard sample is derived from a library. The library is generated by a neural network.

ABEX UPTX: 20000128

EXAMPLE - None given.

=> => fil dpci
FILE 'DPCI' ENTERED AT 15:31:09 ON 29 OCT 2003
COPYRIGHT (C) 2003 THOMSON DERWENT

FILE LAST UPDATED: 24 OCT 2003 <20031024/UP>
PATENTS CITATION INDEX, COVERS 1973 TO DATE

>>> LEARNING FILE LDPCI AVAILABLE <<<

=> d all

L156 ANSWER 1 OF 1 DPCI COPYRIGHT 2003 THOMSON DERWENT on STN
AN 2002-645691 [70] DPCI
DNN N2002-510498 DNC C2002-182410
TI Generating amino acid sequences representative of desired polypeptide, by computationally generating proteolytic cleavage products, analyzing and selecting the set of products, thus generating amino acid sequences.

DC B04 D16 S03 T01
IN **KATZ, E I**
PA (KATZ-I) KATZ E I
CYC 28
PI EP 1223534 A1 20020717 (200270)* EN 124p G06F019-00
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR
US 2002137119 A1 20020926 (200270) G06G007-48
JP 2002360278 A 20021217 (200312) 250p C12N015-09
ADT EP 1223534 A1 EP 2002-75095 20020111; US 2002137119 A1 US 2001-982172 20011019; JP 2002360278 A JP 2002-4906 20020111
PRAI US 2001-982172 20011019; IL 2001-140881 20010114
IC ICM C12N015-09; G06F019-00; G06G007-48
ICS C07K001-12; C07K002-00; C07K016-18; C12M001-34; C12P021-06; C12P021-08; C12Q001-37; G01N033-53; G01N033-68; G01N037-00; G06G007-58
FS CPI EPI

CTCS CITATION COUNTERS

PNC.DI	0	Cited Patents Count (by inventor)
PNC.DX	4	Cited Patents Count (by examiner)
IAC.DI	0	Cited Issuing Authority Count (by inventor)
IAC.DX	1	Cited Issuing Authority Count (by examiner)
PNC.GI	0	Citing Patents Count (by inventor)
PNC.GX	0	Citing Patents Count (by examiner)
IAC.GI	0	Citing Issuing Authority Count (by inventor)
IAC.GX	0	Citing Issuing Authority Count (by examiner)
CRC.I	0	Cited Literature References Count (by inventor)
CRC.X	5	Cited Literature References Count (by examiner)

CDP CITED PATENTS UPD: 20031006

Cited by Examiner

CITING PATENT	CAT	CITED PATENT	ACCNO
EP 1223534	A	A WO 9325700	A 1994-007557/01
		PA: (SUPE-N) INST SUPERIORE DI SANITA; (SUPE-N) IST SUPERIORE SANITA	
		IN: **CIANFRIGLIA, M**	
		Y WO 9502188	A 1995-066992/09
		PA: (REGC) UNIV CALIFORNIA	
		IN: **JOHANSEN, J S; PRICE, P A**	
		X WO 9964621	A 2000-136848/12
		PA: (UYWI-N) UNIV WINTHROP HOSPITAL; (MAES-I) MAESAKA J K	
		IN: **MAESAKA, J K**	
		Y WO 200024777	A 2000-365109/31
		PA: (REGC) UNIV CALIFORNIA; (MEAR-I) MEARES C F; (ODON-I) O'DONNELL R T; (ROSE-I) ROSE L M;	
		IN: **MEARES, C F; O'DONNELL, R T; ROSE, L M**	

REN LITERATURE CITATIONS UPR: 20031006

Citations by Examiner

CITING PATENT	CAT	CITED LITERATURE

EP 1223534	A	MAKSYUTOV A Z ET AL: "ADEPT: A computer program for prediction of protein antigenic determinants." COMPUTER APPLICATIONS IN THE BIOSCIENCES, vol. 9, no. 3, 1993, pages 291-297, XP001062618 ISSN: 0266-7061
EP 1223534	A	WOLF H ET AL: "AN INTEGRATED FAMILY OF AMINO ACID SEQUENCE ANALYSIS PROGRAMS" COMPUTER APPLICATIONS IN THE BIOSCIENCES, vol. 4, no. 1, 1988, pages 187-192, XP001062935 ISSN: 0266-7061
EP 1223534	A	JAMESON B A ET AL: "THE ANTIGENIC INDEX A NOVEL ALGORITHM FOR PREDICTING ANTIGENIC DETERMINANTS" COMPUTER APPLICATIONS IN THE BIOSCIENCES, vol. 4, no. 1, 1988, pages 181-186, XP001062448 ISSN: 0266-7061
EP 1223534	A	CARTER J MARK: "Epitope prediction methods." 1994 , METHODS IN MOLECULAR BIOLOGY, VOL. 36, PAGE(S) 193-206 , 1994 HUMANA PRESS INC. SUITE 808, 999 RIVERVIEW DRIVE, TOTOWA, NEW JERSEY 07512, USA XP001062308 ISBN: 0-89603-274-4 * page 197, paragraph 2.2. - page 201, paragraph 3. *
EP 1223534	A	Cutter: a tool to generate and analyze proteolytic fragments , copyright 1998-1999 Koen Van Der Straeten, Herve Choplin and Thierry Moreau. PROLYSIS Server, university of Tours, France http://delphi.phys.univ-tours.fr/Prolysis/cutter.html XP002193762

```
=> => fil medline
FILE 'MEDLINE' ENTERED AT 15:33:01 ON 29 OCT 2003

 FILE LAST UPDATED: 28 OCT 2003 (20031028/UP).  FILE COVERS 1958 TO DATE.

 On April 13, 2003, MEDLINE was reloaded.  See HELP RLOAD for details.

 MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the
 MeSH 2003 vocabulary.  See http://www.nlm.nih.gov/mesh/changes2003.html
 for a description on changes.

 This file contains CAS Registry Numbers for easy and accurate
 substance identification.

=> d all tot

L158 ANSWER 1 OF 2     MEDLINE on STN
AN   95211183      MEDLINE
DN   95211183    PubMed ID: 7535161
TI   Epitope mapping of a protein using the Geysen (PEPSCAN) procedure.
AU   Carter J M
CS   Cytogen, Princeton, NJ.
SO   METHODS IN MOLECULAR BIOLOGY, (1994) 36 207-23.  Ref:
     15
     Journal code: 9214969. ISSN: 1064-3745.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
     General Review; (REVIEW)
     (REVIEW, TUTORIAL)
LA   English
FS   Priority Journals
EM   199505
ED   Entered STN: 19950510
     Last Updated on STN: 19960129
```

Entered Medline: 19950504
CT Check Tags: Animal; Human
Antibodies, Monoclonal: IM, immunology
Antigen-Antibody Reactions
Aotus trivirgatus
Computers
Enzyme-Linked Immunosorbent Assay: IS, instrumentation
*Enzyme-Linked Immunosorbent Assay: MT, methods
*Epitopes: CH, chemistry
Immune Sera
*Peptide Mapping
*Peptides: CS, chemical synthesis
Peptides: IM, immunology
*Proteins: IM, immunology
Reproducibility of Results
Sequence Analysis: IS, instrumentation
Sonication
CN 0 (Antibodies, Monoclonal); 0 (Epitopes); 0 (Immune Sera); 0 (Peptides); 0 (Proteins)

L158 ANSWER 2 OF 2 MEDLINE on STN
AN **95211182** MEDLINE
DN **95211182** PubMed ID: **7535160**
TI Epitope prediction methods.
AU **Carter J M**
CS Cytogen, Princeton, NJ.
SO METHODS IN MOLECULAR BIOLOGY, **(1994) 36 193-206.** Ref: 31
Journal code: 9214969. ISSN: 1064-3745.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199505
ED Entered STN: 19950510
Last Updated on STN: 19960129
Entered Medline: 19950504
CT Check Tags: Animal; Human
Amino Acid Sequence
Antigen Presentation
Antigen-Antibody Complex: CH, chemistry
Antigen-Antibody Complex: IM, immunology
Antigen-Antibody Reactions
B-Lymphocyte Subsets: IM, immunology
Chemistry, Physical
*Epitopes
Epitopes: CH, chemistry
Epitopes: IM, immunology
Molecular Sequence Data
Protein Structure, Secondary
Receptors, Antigen, T-Cell: IM, immunology
Structure-Activity Relationship
T-Lymphocyte Subsets: IM, immunology
CN 0 (Antigen-Antibody Complex); 0 (Epitopes); 0 (Receptors, Antigen, T-Cell)

=> => fil hcaplus
FILE 'HCAPLUS' ENTERED AT 15:33:55 ON 29 OCT 2003
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.

FILE COVERS 1907 - 29 Oct 2003 VOL 139 ISS 18
FILE LAST UPDATED: 28 Oct 2003 (20031028/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

=> d all tot

L159 ANSWER 1 OF 2 HCAPLUS COPYRIGHT 2003 ACS on STN
AN 1995:295078 HCAPLUS
DN 122:78543
TI **Epitope** mapping of a protein using the Geysen (PEPSCAN) procedure
AU **Carter, J. Mark**
CS Cytogen, Princeton, NJ, USA
SO Methods in Molecular Biology (Totowa, NJ, United States) (**1994**), **36**(PEPTIDE ANALYSIS PROTOCOLS), 207-23
CODEN: MMBIED; ISSN: 1064-3745
DT Journal
LA English
CC 15-1 (Immunochemistry)
AB The PEPSCAN procedure, which is a variation of solid-phase peptide synthesis, is discussed. It comprises the synthesis and immunochem. assay of hundreds of peptides covalently linked to plastic pins. This technol. represents a major advance in the epitope mapping of protein antigens because of its ability to create the large nos. of overlapping peptides needed for complete epitope mapping.
ST protein antigen epitope mapping Geysen PEPSCAN
IT Immunoassay
(epitope mapping of proteins by Geysen PEPSCAN procedure)
IT Antigens
Peptides, properties
Proteins, properties
RL: PRP (Properties)
(epitope mapping of proteins by Geysen PEPSCAN procedure)

L159 ANSWER 2 OF 2 HCAPLUS COPYRIGHT 2003 ACS on STN
AN 1995:295077 HCAPLUS
DN 122:75633
TI **Epitope** prediction methods
AU **Carter, J. Mark**
CS Cytogen, Princeton, NJ, USA
SO Methods in Molecular Biology (Totowa, NJ, United States) (**1994**), **36**(PEPTIDE ANALYSIS PROTOCOLS), **193**-206
CODEN: MMBIED; ISSN: 1064-3745
DT Journal; General Review
LA English
CC 9-0 (Biochemical Methods)
Section cross-reference(s): 15
AB A review with 31 refs. B-cell epitopes, antibody-antigen complexes,

hydrophilicity, T-cell epitope prediction methods, etc., are described.
ST review epitope prediction method
IT Animal cell
(epitope; epitope prediction methods)

=> d his

(FILE 'HOME' ENTERED AT 13:25:22 ON 29 OCT 2003)
DEL HIS

FILE 'HCAPLUS' ENTERED AT 13:26:38 ON 29 OCT 2003
E KATZ E/AU
L1 107 S E3,E7
L2 3 S E46,E47
L3 110 S L1,L2
L4 3 S L3 AND P/DT
L5 1 S L4 AND (G06F OR A61K OR C08K)/IC,ICM,ICS
E POLYPEPTIDE/CT
E E10+ALL
L6 184 S E1
E E2+ALL
L7 112373 S E1
E POLYPEPTIDE/CW
L8 835 S E3,E5
E PEPTIDE/CW
L9 120787 S E3,E4
L10 121587 S L6-L9
L11 469637 S PEPTIDE OR POLYPEPTIDE OR POLY PEPTIDE
L12 9 S L3 AND L10,L11
E MICROARRAY/CT
E E4+ALL
L13 13524 S E5,E6,E4+NT
E E3+ALL
L14 14096 S E2+NT
E E8+ALL
L15 2625 S E3,E2
L16 1970 S E2+NT
E E13+ALL
E ARRAY/CT
E MICROARRAY/CW
L17 12947 S E3
L18 2474 S L10,L11 AND L13-L17
L19 5078 S L10,L11 AND ?ARRAY?
L20 5182 S L18,L19
L21 79 S L10,L11 AND COMPUTATIONAL ANALYSIS
L22 2735 S L10,L11 AND COMPUT?(L)ANALY?
E L10,L11 AND ANTIBOD?
L23 63470 S L10,L11 AND ANTIBOD?
L24 2265 S L23 AND L20
L25 383 S L23 AND L21,L22
E DATABASE/CT
E E5+ALL
L26 93 S L23 AND E1
E E10+ALL
L27 112 S L23 AND E2-E7,E1+NT
L28 256 S L23 AND (E68+NT OR E72+NT OR E73+NT)
L29 3049 S L21,L22,L25-L28
L30 198 S L29 AND L20
E E68+ALL
E COMPUT/CT
E E5+ALL
L31 0 S L23 AND E2

```
                E COMPUT/CT
L32          327 S L23 AND (E26+NT OR E28+NT)
                E E51+ALL
L33           52 S L23 AND E4,E5,E3
L34          117 S L32,L33 AND L20
L35          223 S L30,L34
L36            2 S L35 AND PROTEOLY?
L37            1 S L3 AND L23
L38            1 S L37 AND L25-L36

     FILE 'REGISTRY' ENTERED AT 13:56:42 ON 29 OCT 2003
L39            9 S 506-68-3 OR 30211-77-9 OR 9004-06-2 OR 9002-04-4 OR 9002-07-7

     FILE 'HCAPLUS' ENTERED AT 13:56:56 ON 29 OCT 2003
L40           12 S L39 AND L35
L41           15 S L35 AND (CYANOGEN BROMIDE OR 2 NITRO 5 THIOCYANOBENZOATE OR E
L42           66 S L35 AND ?ENZYM?
L43           72 S L36,L40-L42
L44           54 S L43 AND (BIOCHEM?(L)METHOD?)/SC,SX
                SEL DN AN 17 22 25 33 36 45 50
L45            7 S L44 AND E1-E21
L46            8 S L5,L36-L38,L45 AND L1-L38,L40-L45
L47           12 S L3 AND (BIOCHEM?(L)METHOD?)/SC,SX
L48            2 S L3 AND G01N/IC,ICM,ICS
L49            2 S L3 AND L13-L38
L50            1 S L46 AND L47-L49
L51            8 S L46,L50
L52           90 S L3 NOT L47-L51,L12

     FILE 'BIOSIS' ENTERED AT 14:13:45 ON 29 OCT 2003
                E KATZ E/AU
L53          282 S E3
L54           34 S L53 AND ?PEPTIDE?
L55           24 S L53 AND ?PROTEIN?
                E PEPTIDE/CC
                E POLYPEPTIDE/CC
                E PROTEIN/CC
                E A/CC
L56          142 S L53 AND (13012 OR 10054 OR 10064)/CC
L57          146 S L54,L55,L56
L58            1 S L57 AND 00530/CC
L59            1 S L57 AND 04500/CC
L60            0 S L57 AND ?ARRAY?
L61            0 S L57 AND L39
L62           40 S L57 AND (CYANOGEN BROMIDE OR 2 NITRO 5 THIOCYANOBENZOATE OR E
L63            2 S L57 AND ?PROTEOL?
L64            4 S L53 AND P/DT

     FILE 'MEDLINE' ENTERED AT 14:21:34 ON 29 OCT 2003
                E KATZ E/AU
L65          357 S E3
L66           78 S L65 AND (?PEPTIDE? OR ?PROTEIN?)
L67          118 S L65 AND D12./CT
L68          139 S L66,L67
L69            0 S L68 AND ?ARRAY?
L70           11 S L68 AND L1./CT
                SEL DN AN 8
L71            1 S L70 AND E1-E3
                E MICROARRAY/CT
                E E4+ALL
                E E2+ALL
L72          220 S E7+NT
                E MICROARRAY/CT
```

```
                E E12+ALL
                E COMPUT/CT
                E E10+ALL
L73          3946 S E6+NT
L74            11 S L72 AND L73
                E SEQUENCE ANALYSIS/CT
                E E19+ALL
L75          9201 S E5+NT
L76            98 S L75 AND L73
L77            15 S L75 AND L72
L78           120 S L74,L76,L77
L79            96 S L78 AND D12./CT
L80          6959 S L39
L81       1153897 S CYANOGEN BROMIDE OR 2 NITRO 5 THIOCYANOBENZOATE OR ELASTASE O
L82          4780 S L80,L81 AND L73,L75
L83             1 S L82 AND L72
L84            13 S L82 AND L78
L85            13 S L83,L84
L86          1109 S ANTIBODIES+NT/CT AND L73,L75
L87          1015 S L86 AND D12./CT
L88             3 S L87 AND L72
L89            16 S L85,L88

     FILE 'HCAPLUS' ENTERED AT 14:32:19 ON 29 OCT 2003
L90             1 S CIANFRIGLIA ?/AU AND WO9325700/PN
L91             1 S JAMESON ?/AU AND 1988/PY AND (4 AND 1 AND 181)/SO
L92             1 S MAKSYUTOV ?/AU AND 1993/PY AND (9 AND 3 AND 291)/SO
L93             3 S (WO9502188 OR WO200024777 OR WO9964621)/PN
L94             1 S WOLF ?/AU AND 1988/PY AND (4 AND 1 AND 187)/SO
L95             7 S L90-L94 NOT L51

     FILE 'MEDLINE' ENTERED AT 14:36:54 ON 29 OCT 2003
                SEL DN AN L89 3 4 8 11
L96             4 S L89 AND E1-E12
                E PEPTIDES/CT
L97        876612 S E3+NT
L98         52093 S L97 AND ANTIBODIES+NT/CT
L99         11045 S L98 AND ENZYMES+NT/CT
L100        11542 S L98 AND L80,L81
L101         1066 S L98 AND PROTEOLY?
L102        16976 S L99-L101
L103           59 S L102 AND ?ARRAY?
L104            2 S L102 AND L73
L105           60 S L103,L104
L106            2 S L73 AND L102
L107           60 S L105,L106
L108         4654 S L102 AND L1./CT
L109           24 S L108 AND L107
                SEL DN AN 1 4
L110            2 S L109 AND E1-E6
L111            6 S L96,L110
L112           36 S L107 NOT L109
                SEL DN AN 6 13 14 17 18
L113            5 S L112 AND E7-E21
L114           11 S L111,L113 AND L65-L89,L96-L113
L115           12 S L89 NOT L114

     FILE 'MEDLINE' ENTERED AT 14:56:49 ON 29 OCT 2003

     FILE 'WPIX' ENTERED AT 14:56:57 ON 29 OCT 2003
                E KATZ E/AU
L116           54 S E3,E8
L117            4 S L116 AND G06F/IC,ICM,ICS,ICA,ICI
```

```
L118           4 S L116 AND T?/DC
L119           4 S L116 AND T?/MC
L120           5 S L117-L119
L121           1 S L120 AND C07K/IC,ICM,ICS,ICA,ICI
L122           1 S L116 AND C07K/IC,ICM,ICS,ICA,ICI
L123          11 S L116 AND G01N/IC,ICM,ICS,ICA,ICI
L124           7 S L116 AND S03-E14H?/MC
L125           1 S L120-L124 AND ?PEPTIDE?/BIX
L126     1342968 S T01/DC OR (G06G OR G06F)/IC,ICM,ICS OR T?/MC
L127     1343074 S (B11-C08F3 OR C11-C08F3)/MC OR L126
L128         817 S L127 AND (C07K/IC,ICM,ICS OR (B04-C01? OR C04-C01?)/MC)
L129         198 S L128 AND (B04-G01 OR C04-G01 OR B04-B04C OR C04-B04C)/MC
L130         641 S L127 AND (B04-N04? OR C04-N04?)/MC
L131         118 S L130 AND (B04-G01 OR C04-G01 OR B04-B04C OR C04-B04C)/MC
L132         122 S L120,L131
L133          91 S L128 AND (B11-C07A OR C11-C07A)/MC
L134         193 S L132,L133
L135         649 S (B11-C08F4 OR C11-C08F4)/MC
L136         190 S L135 AND (B04-G01 OR C04-G01 OR B04-B04C OR C04-B04C)/MC
L137         200 S L135 AND (B04-N04? OR C04-N04?)/MC
L138         523 S L134,L136,L137
L139         546 S D05-H11/MC AND L126,L127,L135
L140         236 S L139,L138 AND L81/BIX
L141          97 S L139,L138 AND (B11-C08E3 OR C11-C08E3)/MC
L142         210 S L138,L139 AND C12P/IC,ICM,ICS
L143         363 S L138,L139 AND C12Q/IC,ICM,ICS
L144         397 S L138,L139 AND C12N/IC,ICM,ICS
L145          42 S L138,L139 AND C12M/IC,ICM,ICS
L146         630 S L141-L145,L140
L147         478 S L146 AND (PEPTIDE? OR POLYPEPTIDE? OR POLY PEPTIDE?)/BIX
L148         479 S L146 AND ?PEPTIDE?/BIX
L149         479 S L147,L148
L150         123 S L149 AND (COMPUT?(L)ANALY?)/BIX
L151          25 S L150 AND ?ARRAY?/BIX
L152          25 S L151 AND ANTIBOD?/BIX
L153          13 S L152 AND L140
                 SEL DN AN 8 9 13
L154           3 S E1-E8 AND L153
L155           3 S L154 AND L116-L154

     FILE 'WPIX' ENTERED AT 15:30:35 ON 29 OCT 2003

     FILE 'DPCI' ENTERED AT 15:30:45 ON 29 OCT 2003
                 E KATZ E/AU
L156           1 S E7

     FILE 'DPCI' ENTERED AT 15:31:09 ON 29 OCT 2003

     FILE 'MEDLINE' ENTERED AT 15:32:20 ON 29 OCT 2003
L157          15 S CARTER ?/AU AND 1994/PY AND (36 OR 193 OR 197)/SO
                 SEL DN AN 2 3
L158           2 S L157 AND E1-E6

     FILE 'MEDLINE' ENTERED AT 15:33:01 ON 29 OCT 2003

     FILE 'HCAPLUS' ENTERED AT 15:33:13 ON 29 OCT 2003
L159           2 S CARTER ?/AU AND 1994/PY AND (36 OR 193 OR 197)/SO AND EPITOP?

     FILE 'HCAPLUS' ENTERED AT 15:33:55 ON 29 OCT 2003

=>
```